52

#### Raw Sequence Listing

Au 1806

06/27/93

# Patent Application US/07/952,640

1		SEQUENCE LISTING
2		
3 4 5	(1) GENE	ral information: — See $\gamma$
6 7 8	(i)	APPLICANT: CROWE, JAMES SCOTT LEWIS, ALAN PETER
9	(ii)	TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
11 12	(iii)	NUMBER OF SEQUENCES: 46
13 14 15 16 17 18 19	(iv)	CORRESPONDENCE ADDRESS:  (A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  (B) STREET: 555 THIRTEENTH ST. N.W.  (C) CITY: WASHINGTON  (D) STATE: D. C.  (E) COUNTRY: U.S.  (F) ZIP: 20004
21 22 23 24 25 26	(v)	COMPUTER READABLE FORM:  (A) MEDIUM TYPE: Floppy disk  (B) COMPUTER: IBM PC compatible  (C) OPERATING SYSTEM: PC-DOS/MS-DOS  (D) SOFTWARE: Patentin Release #1.0, Version #1.25
27 28 29 30 31	(vi)	CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER: US 07/952640  (B) FILING DATE: 01-DEC-1992  (C) CLASSIFICATION:
32 33 34 35 36	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: ERNST, BARBARA G (B) REGISTRATION NUMBER: 30,377 (C) REFERENCE/DOCKET NUMBER: 1808-118
37 38 39 40 41	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (202) 783-6040 (B) TELEFAX: (202) 783-6031
42	(2) INF	ORMATION FOR SEQ ID NO:1:
44 45 46 47 48 49	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear
50 51	(ii)	MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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53 54	GACATTCAGC TGACCCAGTC TCCA	24
55 56	(2) INFORMATION FOR SEQ ID NO:2:	
57 58	(i) SEQUENCE CHARACTERISTICS:	
59	(A) LENGTH: 24 base pairs	
60	(B) TYPE: nucleic acid	
61	(C) STRANDEDNESS: single	
62	(D) TOPOLOGY: linear	
63	(-,	
64	(ii) MOLECULE TYPE: DNA (genomic)	
65	(30.32.20)	
66	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
67	,,	
68	GATCAAGCTT CTAACACTCT CCCC	24
69		
70	(2) INFORMATION FOR SEQ ID NO:3:	
71		
72	(i) SEQUENCE CHARACTERISTICS:	
73	(A) LENGTH: 34 base pairs	
74	(B) TYPE: nucleic acid	
75	(C) STRANDEDNESS: single	
76	(D) TOPOLOGY: linear	
77		
78	(ii) MOLECULE TYPE: DNA (genomic)	
79		
80	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
81	01 EC1 1 00EE 01 01 ET ET 02 E 02 0 E	2.4
82	GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA	34
83 84	(2) INFORMATION FOR SEQ ID NO:4:	
85	(2) INFORMATION FOR BEQ ID NO.4:	
86	(1) SEQUENCE CHARACTERISTICS:	
87	(A) LENGTH: 16 base pairs	
88	(B) TYPE: nucleic acid	
89	(C) STRANDEDNESS: single	
90	(D) TOPOLOGY: linear	
91		
92	(ii) MOLECULE TYPE: DNA (genomic)	
93		
94	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
95		
96	AACAGCTATG ACCATG	16
97		
98	(2) INFORMATION FOR SEQ ID NO:5:	
99		
100	(i) SEQUENCE CHARACTERISTICS:	
101	(A) LENGTH: 17 base pairs	
L02	(B) TYPE: nucleic acid	
L03	(C) STRANDEDNESS: single	
L04	(D) TOPOLOGY: linear	

#### Raw Sequence Listing

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105		
106	(ii) MOLECULE TYPE: DNA (genomic)	
107	(,,	
108	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
109	(AI) DEGUEAGE DESCRIPTION. DEG ID NO. 3.	
110	GTTTTCCCAG TCACGAC	17
	GITTECCAG FCACGAC	17
111	(0)	
112	(2) INFORMATION FOR SEQ ID NO:6:	
113		
114	(i) SEQUENCE CHARACTERISTICS:	
115	(A) LENGTH: 20 baee paire	
116	(B) TYPE: nucleic acid	
117	(C) STRANDEDNESS: eingle	
118	(D) TOPOLOGY: linear	
119		
120	(ii) MOLECULE TYPE: DNA (genomic)	
121		
122	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
123		
124	GCGTCAGGGT GCTGCTGAGG	20
125		
126	(2) INFORMATION FOR SEQ ID NO:7:	
127	(2) INFORMATION FOR SEQ ID NO. / .	
128	(i) GEOURNAR GUARAGERT GEORGE	
	(i) SEQUENCE CHARACTERISTICS:	
129	(A) LENGTH: 20 baee paire	
130	(B) TYPE: nucleic acid	
131	(C) STRANDEDNESS: single	
132	(D) TOPOLOGY: linear	
133		
134	(ii) MOLECULE TYPE: DNA (genomic)	
135		
136	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
137		
138	GGCGGGAAGA TGAAGACAGA	20
139		
140	(2) INFORMATION FOR SEQ ID NO:8:	
141	(-,	
142	(i) SEQUENCE CHARACTERISTICS:	
143	(A) LENGTH: 20 base pairs	
144	(B) TYPE: nucleic acid	
145	(C) STRANDEDNESS: single	
	The state of the s	
146	(D) TOPOLOGY: linear	
147		
148	(ii) MOLECULE TYPE: DNA (genomic)	
149		
150		
151		
152	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
153		
154	TTCAGCAGGC ACACAACAGA	20
155		
156	(2) INFORMATION FOR SEQ ID NO:9:	

# Raw Sequence Listing

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157																		
158		(i)	) SE	QUEN	CE C	HARA	CTER	ISTI	CS:									
159			()	A) Li	ENGT:	H: 10	6 <b>1</b> 7 1	base	pai	rs								
160						nuc:												
161						DEDNI			h									
162			(1	D) T(	OPOL	OGY:	lin	ear										
163																		
164		(ii)	MO	LECU	LE T	YPE:	cDN2	A.						r				
165																		
166		(iii)	HY	POTH	ETIC	AL: 1	10											
167		,, ,																
168		(1V)	AN'	ri-si	ense	: NO												
169																		
170 171		/2		. m 270-1	m .													
172		(1X	) FE			vev.	~4~											
173						KEY:		_	cide									
174			()	ידר נים	JCAT.	ION:	35.	. 92										
175		(dae)	FE	י מדדם ו	₽.													
176		( +. ~.				KEY:	mat	non	-430									
177						ION:												
178			(,	יבו ,כ	JUAI.	LOIN	23.	. 170.	,									
179		(ix)	FE	וקנזים	R•													
180		,				KEY:	CDS											
181						ION:		.146	5									
182			,-	-,														
183																		
183 184		(xi)	SE	QUEN	CE DI	ESCR:	IPTIO	on: a	SEQ :	ID N	0:9:							
		(xi)	SE	QUEN	CE DI	ESCR:	IPTIO	on: a	SEQ :	ID N	0:9:							
184	TCT		·	-					_			AC TO	GG A	CC TO	GG A	3G	52	
184 185	TCT		·	-					_	CC A	IG G	AC To					52	
184 185 186	TCT		·	-					_	CC A!	IG G			hr T			52	
184 185 186 187 188	TCT		·	-					_	CC A!	IG G			hr T	rp A		52	
184 185 186 187 188 189	TTC	AAAG/	AAG (	GTG	rggg; GTG	ag cz Gca	ACAG( GCA	CTCA!	r CA(	CC A: Mc -: GGT	TG GA et Aa 19 GTC	ep Ti CAG	rp T) TCC	hr T: -: CAG	rp A: 15 ATG	rg CAG		
184 185 186 187 188 189 190	TTC	AAAG/	AAG (	GTG Val	rggg; GTG	ag cz Gca	ACAG( GCA	CTCA!	r cad	CC A: Mc -: GGT	TG GA et Aa 19 GTC	sp Ti	rp T) TCC	hr T: -: CAG Gln	rp A: 15 ATG	rg CAG		
184 185 186 187 188 189 190 191	TTC	AAAG/	AAG (	GTG	rggg; GTG	ag cz Gca	ACAG( GCA	CTCA!	r cad	CC A: Mc -: GGT	TG GA et Aa 19 GTC	ep Ti CAG	rp T) TCC	hr T: -: CAG	rp A: 15 ATG	rg CAG		
184 185 186 187 188 189 190 191 192	TTC Phe	AAAGA CTC Leu	AAG (	GTG Val	FGGG GTG Val	AG CA GCA Ala	GCA GCA Ala	GCT Ala	ACA Thr	GGT GGT	TG GZ et Ag 19 GTC Val	EP TI	TCC Ser	CAG Gln 1	rp A: 15 ATG Met	rg CAG Gln	100	
184 185 186 187 188 189 190 191 192 193	TTC Phe GTG	CTC Leu GTG	TTT Phe	GTG Val -10	GTG Val	GCA Ala GCT	GCA GCA Ala GAA	GCT Ala	ACA Thr -5	GGT GGT GAG	TG GE et As 19 GTC Val	CAG Gln GGG	TCC Ser	CAG Gln 1	rp A: 15 ATG Met	CAG Gln ACG		
184 185 186 187 188 189 190 191 192 193 194 195	TTC Phe GTG	CTC Leu GTG Val	TTT Phe	GTG Val -10	GTG Val	GCA Ala GCT	GCA Ala GAA Glu	GCT Ala	ACA Thr -5	GGT GGT GAG	TG GE et As 19 GTC Val	CAG Gln GGG Gly	TCC Ser	CAG Gln 1	rp A: 15 ATG Met	CAG Gln ACG	100	
184 185 186 187 188 189 190 191 192 193 194 195	TTC Phe GTG	CTC Leu GTG	TTT Phe	GTG Val -10	GTG Val	GCA Ala GCT	GCA GCA Ala GAA	GCT Ala	ACA Thr -5	GGT GGT GAG	TG GE et As 19 GTC Val	CAG Gln GGG	TCC Ser	CAG Gln 1	rp A: 15 ATG Met	CAG Gln ACG	100	
184 185 186 187 188 189 190 191 192 193 194 195 196	TTC Phe GTG Val	CTC Leu GTG Val	TTT Phe CAG	GTG Val -10 TCT Ser	GTG Val GGG Gly	GCA Ala GCT Ala	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG	GGT GGT Gly AAG Lys	rg Gz et A, 19 GTC Val CCT Pro	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr	100	
184 185 186 187 188 189 190 191 192 193 194 195 196 197	TTC Phe GTG Val	CTC Leu GTG Val 5	TTT Phe CAG Gln	GTG Val -10 TCT Ser	GTG Val GGG Gly	GCA Ala GCT Ala	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG Lys	GGT GGT GLY AAG LYS	GTC Val	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr	100	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198	TTC Phe GTG Val	CTC Leu GTG Val 5	TTT Phe CAG Gln	GTG Val -10 TCT Ser	GTG Val GGG Gly	GCA Ala GCT Ala TCT Ser	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG Lys	GGT GGT GLY AAG LYS	GTC Val	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser	100	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	TTC Phe GTG Val	CTC Leu GTG Val 5	TTT Phe CAG Gln	GTG Val -10 TCT Ser	GTG Val GGG Gly	GCA Ala GCT Ala	GCA Ala GAA Glu 10	GCT Ala GTA Val	ACA Thr -5 AAG Lys	GGT GGT GLY AAG LYS	GTC Val	CAG Gln GGG Gly 15	TCC Ser TCC Ser	CAG Gln 1 TCG Ser	ATG Met GTG Val	CAG Gln ACG Thr	100	
184 185 186 187 188 190 191 192 193 194 195 196 197 198 199 200 201	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5 TCC Ser	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser	GTG Val GGG Gly GCA Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly	ACA Thr -5 AAG Lys ACC Thr	GGT GGT Gly AAG Lys TTC Phe	GTC Val  CCT Pro  AGC Ser	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT TYr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100 148 196	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5 TCC Ser	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly CAA	ACA Thr -5 AAG Lys ACC Thr	GGT Gly  AAG Lys  TTC Phe	GTC Val  CCT Pro  AGC Ser 30	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT TYr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5 TCC Ser	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala GCC Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly CAA	ACA Thr -5 AAG Lys ACC Thr	GGT Gly  AAG Lys  TTC Phe  CTT Leu	GTC Val  CCT Pro  AGC Ser 30	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT TYr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100 148 196	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204	TTC Phe GTG Val GTC Val 20	CTC Leu GTG Val 5 TCC Ser	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala	GCA Ala GCT Ala TCT Ser 25	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly CAA	ACA Thr -5 AAG Lys ACC Thr	GGT Gly  AAG Lys  TTC Phe	GTC Val  CCT Pro  AGC Ser 30	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT TYr	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35	100 148 196	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu GTG Val TCC Ser GTG Val	TTT Phe CAG Gln TGC Cys	GTG Val -10 TCT Ser AAG Lys	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT	GCA Ala GAA Glu 10 GGA Gly	GCT Ala GTA Val GGC Gly CAA	ACA Thr -5 AAG Lys ACC Thr	GGT Gly  AAG Lys  TTC Phe  CTT Leu  45	GTC Val  CCT Pro  AGC Ser 30  GAG Glu	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT Tyr ATG Met	CAG Gln 1 TCG Ser GCT Ala	ATG Met GTG Val	CAG Gln ACG Thr AGC Ser 35 ATC	100 148 196 244	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu  GTG Val  TCC Ser  GTG Val	TTT Phe CAG Gln TGC Cys CGA Arg	GTG Val -10 TCT Ser AAG Lys CAG Gln	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT Pro	GCA Ala GAA Glu 10 GGA Gly GGA Gly	GCT Ala GTA Val GGC Gly CAA Gln	ACA Thr -5 AAG Lys ACC Thr GGG Gly	GGT Gly  AAG Lys  TTC Phe  CTT Leu  45	GTC Val  CCT Pro  AGC Ser  30  GAG GIU	CAG Gln GGG Gly 15 AAC Asn TGG Trp	TCC Ser TCC Ser TAT Tyr ATG Met	CAG Gln 1 TCG Ser GCT Ala GGA Gly	ATG Met GTG Val ATC Ile GGG Gly 50 GGC	CAG Gln ACG Thr AGC Ser 35 ATC Ile	100 148 196	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	TTC Phe GTG Val GTC Val 20 TGG Trp	CTC Leu  GTG Val  TCC Ser  GTG Val	TTT Phe CAG Gln TGC Cys CGA Arg	GTG Val -10 TCT Ser AAG Lys CAG Gln	GTG Val GGG Gly GCA Ala GCC Ala 40	GCA Ala GCT Ala TCT Ser 25 CCT Pro	GCA Ala GAA Glu 10 GGA Gly GGA Gly	GCT Ala GTA Val GGC Gly CAA Gln	ACA Thr -5 AAG Lys ACC Thr GGG Gly	GGT Gly  AAG Lys  TTC Phe  CTT Leu  45	GTC Val  CCT Pro  AGC Ser  30  GAG GIU	CAG Gln GGG Gly 15 AAC Asn	TCC Ser TCC Ser TAT Tyr ATG Met	CAG Gln 1 TCG Ser GCT Ala GGA Gly	ATG Met GTG Val ATC Ile GGG Gly 50 GGC	CAG Gln ACG Thr AGC Ser 35 ATC Ile	100 148 196 244	

#### Raw Sequence Listing

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209																		
210		ACG						_					-				3	40
211	Val	Thr		Thr	Ala	Asp	Lys		Thr	Ser	Thr	Ala		Met	Glu	Leu		
212			70					75					80					
213 214	a cerr	100	ara	3.03	m am	<b>G2 G</b>	a. a	100	000	ara	m a m	ma a	mar.	aaa	3.03	CIS III	,	
215		AGC Ser												-			3	88
215	1111	85	пеп	ALG	Per	GIU	90	1111	ATG	Val	ığı	95	Cys	АТА	1111	Авр		
217		03					20					,,						
218	CGC	TAC	AGG	CAG	GCA	AAT	TTT	GAC	CGG	GCC	CGG	GTT	GGC	TGG	TTC	GAC	4	36
219		Tyr															-	
220	100		3			105			5		110					115		
221																		
222	CCC	TGG	GGC	CAG	GGC	ACC	CTG	GTC	ACC	GTC	TCC	TCA	GCC	TCC	ACC	AAG	4	84
223	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lye		
224					120					125					130			
225																		
226	GGC	CCA	TCG	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	5	32
227	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lye	Ser	Thr	Ser	Gly		
228				135					140					145				
229																	_	
230		ACA															5	80
231	GIY	Thr		Ala	Leu	СТĀ	Cye		Val	Lye	Aep	lyr		Pro	GIu	Pro		
232			150					155					160					
233 234	OTO.	ACG	CTC	TOO	TOO	330	ሞርን	ccc	ccc	CHT CI	1. CC	N.C.C	ccc	CTC.	CZ C	3.00	6	28
235		Thr												_			٠	20
236	VAI	165	VOI	Ser	TIP	VOIT	170	GLY	WI.	nen	+ ***	175	GLY	Val	1110	+111		
237		-05					-,0					1,5						
238	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	6	76
239		Pro																
240	180					185			•		190					195	•	
241																		
242	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG	ACC	TAC	ATC	TGC	AAC	7	24
243	Va1	Thr	Va1	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Сув	Asn		
244					200					205					210			
245																		
246		AAT															7	72
247	Val	Aen	Hie	-	Pro	Ser	Aen	Thr	_	Val	Asp	Lys	Lys		Glu	Pro		
248				215					220					225				
249											~~~		~~~		~~~	<b>411</b>		
250		TCT												_		_	8	20
251 252	гле	Ser		Aep	гле	TUE	HIS		<b>∟</b> y8	PFO	PFO	СУВ	240	ATG	PFO	GIU		
253			230					235					4 T U					
253	ייידיי	CTG	aca	CCD	CCG	TCA	GTC	ጥጥር	СТС	ттс	ccc	CCA	444	CCC	AAC	GAC	я	68
255		Leu	_															
256		245	1	1			250					255			_1.0	<b>F</b>		
257																		
258	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	9	16
259	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Va1	Thr	Суе	Va1	Val	Val	Aep		
260	260					265					270	-				275		

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261																	
262			_													GGC	964
263	Val	Ser	His	Glu		Pro	Glu	Val	Lys		Asn	$\mathtt{Trp}$	Tyr	Val	Asp	Gly	
264					280					285					290		
265																	
266				_											TAC		1012
267	Val	Glu	Val		Asn	Ala	Lys	Thr	-	Pro	Arg	Glu	Glu		Tyr	Asn	
268				295					300					305			
269																	
270									-						GAC		1060
271	ser	Thr		Arg	Val	Val	ser		Leu	Thr	Val	Leu		GIn	Asp	Trp	
272			310					315					320				
273	ama	3.307	~~~		a. a	m> a		maa		ama	maa			~~~	am a	992	1100
274															CTC		1108
275	теп		GTA	гав	GIU	Tyr		Cys	гав	val	ser		гĀв	ALA	Leu	Pro	
276		325					330					335					
277	~~~			~~~													
278															CGA		1156
279		Pro	тте	GIU	гав		тте	ser	гав	АТА		GIA	GIn	Pro	Arg		
280	340					345					350					355	
281	001	~~~	am a	m 2 cs	3.00	ama	999	993	maa	999	~ m	<b>~</b> 3 ~	ama	3.00	330	330	1204
282															AAG		1204
283	Pro	GIn	Val	Tyr		тел	Pro	Pro	ser		Asp	GIU	ьeu	Thr	Lys	Asn	
284					360					365					370		
285	a. a	-		ama		maa	ama	-		~~~					a. a		1050
286															GAC		1252
287	GIN	vaı	ser		Thr	Cys	гел	vaı		GTĀ	Pue	ıyr	Pro		Asp	TTE	
288				375					380					385			
289	~~~	ama	~~	m a a	~~~			~~~	~~	-	~~~			m = 0		3.00	1200
290															AAG		1300
291 292	ALA	val		Trp	GIU	ser	ABII		GIII	Pro	GIU	ABII		TAL	Lys	THE	
292			390					395					400				
293	እሮሮ	COT	ccc	Cuttica	CTTC	CAC	TOO	CAC	cac	TOO	, 1011/C	ጥጥረ	CTC	ሞአሮ	AGC	33C	1348
295															Ser		1340
296	1111	405	PLO	Val	пеп	ABP	410	APP	GTĀ	Ser	FIIG	415	пеп	TÄT	261	цув	
297		100					410					117					
298	כיייכ	a cc	CTC	CAC	AAC	ACC	A CC	таа	CAG	CAG	ccc	AAC	GTC	TTC	TCA	TGC	1396
299														_	Ser		1330
300	420		V W I	wp	<b>1</b> 170	425	9		01	01	430	*****	<b>7</b> CA T			435	
301	120					127					150					100	
302	TCC	GTG	ATG	САТ	GAG	GCT	СТС	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	1444
303															Ser		
304	_ ~_				440					445	-2-		~	-1~	450		
305																	
306	TCC	CTG	TCT	CCG	GGT	AAA	TGAC	TGC	SAC (	igcc(	GCA 2	AG CO	adda	GCTC	2		1492
307			Ser					(						\	_		
308	~~~	~~	~~-	455	1	-1 ~											
309																	
310	CCG	GGCT	CTC (	GCGG1	rcgc:	AC GZ	AGGAT	rgcti	r GGG	CACG	CACC	CCG1	CGTAC	CAT	ACTTO	cceee	1552
311		,															
312	CGC	CCAG	CAT	GAAI	ATAAZ	AG C	ACCC	AGCGG	TG(	CCT	GGC	CCC	rgcgi	AAA I	AAAA	AAAAA	1612
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313

#### Raw Sequence Listing

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213																	
314	AAA	A.A.															1617
315	(2)	INI (	FORM	ATIO	N FO	R SE	Q ID	NO:	10:								
316							-										
317			(1)	SEQU	ENCE	CHAI	RACTI	RRTS	TTCS	-							
318			`-, .		) LE						-						
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325																	
326	Met	Asp	Tro	Thr	Tro	Ara	Phe	Leu	Phe	Val	Val	Ala	Ala	Ala	Thr	Glv	
327	-19		1		-15	5				-10					-5	2	
328															-		
	3	~1 -		~1 -	<b>36- L</b>	~1_	1	7	~1_	<b>a</b>	~1		~1	7		•	
329	Val	GIN	Ser	Gln	met	GIN	Val		GIN	Ser	GIA	ALA		var	гÃв	гÃВ	
330				1				5					10				
331																	
332	Pro	Gly	Ser	Ser	Val	Thr	Val	Ser	Сув	Lys	Ala	Ser	Gly	Gly	Thr	Phe	
333		15					20					25					
334																	
335	Ser	Asn	Tvr	Ala	Ile	Ser	Tro	Val	Arq	Gln	Ala	Pro	Glv	Gln	Glv	Leu	
336	30					35			~		40					45	
337						-											
338	G1.1	Two	Mot	Gly	G1 ve	Tla	Tla	Pro	T.011	Dha	Gl ve	Thr	Dro	The	Tare	Cor	
	GIU	TTD	Mec	Gry	_	110	TT-0	FIG	nea		GLY	T 111	FIO	T 111	-	Per	
339					50					55					60		
340		_				_						_	_	_		_	
341	Gln	Asn	Phe	Gln	GLY	Arg	Val	Thr		Thr	Ala	Asp	Lys		Thr	Ser	
342				65					70					75			
343																	
344	Thr	Ala	His	Met	Glu	Leu	Thr	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
345			80					85					90				
346																	
347	Tvr	Tvr	Cvs	Ala	Thr	Asp	Arg	Tvr	Arg	Gln	Ala	Asn	Phe	Asp	Ara	Ala	
348	-4-	95	-4				100	-4-	3			105			3		
349												_00					
	3	**- 1	a1	m	Dh.		D	m	a1	~1_	<b>~1</b>	ml	<b>.</b>	*** 1	ml	*** 1	
350	_	Val	GTA	Trp	Pne	_	PIO	Trp	GLY	GII	_	THE	Leu	Val	Int		
351	110					115					120					125	
352																	
353	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
354					130					135					140		
355																	
356	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
357		-		145		_	_		150			-	_	155		_	
358																	
359	) an	Тч э	Dhe	Pro	<u>روا به</u>	Dra	₹7≈ T	ጥሎም	₹7a1	Ser	Terr	Aer	Ser	@1 <sub>32</sub>	A1=	T.e.	
	Aap	TAT		FIO	GIU	FIO	Val	165	Val	Ser	тър	Agii		GLY	AIG	пеп	
360			160					T03					170				
361		_						_			_					_	
362	Thr		Gly	Val	His	Thr		Pro	Ala	Val	Leu		Ser	Ser	GLY	Leu	
363		175					180					185					
364																	

# Raw Sequence Listing

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365 366 367	Tyr 190	Ser	Leu	Ser	Ser	Val 195	Val	Thr	Val	Pro	Ser 200	Ser	Ser	Leu	Gly	Thr 205
368 369 370	Glı	n Th	r Ty	r Ile	e Cy≀ 210	s Ası	n Val	l Ası	n Hi	8 Ly: 215	s Pro	o Sei	r Ası	n Thi	г Ly: 220	s Val
371 372 373	Asp	Lys	Lys	Val 225	Glu	Pro	Lys	Ser	Сув 230	Asp	Lys	Thr	His	Thr 235	Сув	Pro
374 375 376	Pro	Сув	Pro 240	Ala	Pro	Glu	Leu	Leu 245	Gly	Gly	Pro	Ser	Val 250	Phe	Leu	Phe
377 378 379		255	Lys			_	260					265				
380 381 382	270		Val			275					280				•	285
383 384 385 386		_	Tyr		290					295			•		300	
387 388 389			Glu	305					310					315		
390 391 392			320 Lys					325	_	-			330			
393 394 395		335	Gln				340				_	345				
396 397 398	350		Leu		Ā	355				_	360					365
399 400 401			Pro		370					375		-			380	_
402 403 404	Glu	_		385	_				390	Œ.				395		
405 406 407	Phe	Phe	400 Leu	Tyr	Ser	Lys	Leu	405 Thr	Val	Asp	Lys	Ser	410 Arg	Trp	Gln	Gln
408 409 410	Gly	415 Asn	Val	Phe	Ser	Сув	420 Ser	Val	Met	His	Glu	425 Ala	Leu	His	Asn	His
411 412 413	430 Tyr	Thr	Gln	Lys	Ser	435 Leu	Ser	Leu	Ser	Pro	440 Gly	Lys				445
414 415 416					450					455						

#### Raw Sequence Listing

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419		(i		_		HARA											
420 421						H: 90		-		8							
422						DEDNI											
423			•	-		OGY:			••								
424			,														
425		(ii	MO:	LECU	LE T	YPE:	CDN	A							•		
426																	
427	(iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO																
428	(iv) ANTI-SENSE: NO																
429																	
430 431																	
431		(ix) FEATURE:															
433	(ix) FEATURE:																
434		(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 32739															
435				-,													
436		(ix	) FE	ATURI	€:												
437						KEY:			tids								
438			(1	3) L	CAT	ION:	89.	.739									
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440		(ix	) FE														
441 442						KEY:			tide								
			(1	2) TV	JUAI.	LON:	34.	. 00									
443																	
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444		(xi	) SEC	OUEN	CE DI	ESCRI	IPTI	ON: S	SEO :	ID N	0:11	•					
		(xi	) SE(	QUEN(	CE DI	escr:	IPTI(	ON: !	SEQ :	ID N	0:11	:					
444 445	CAA		•	_					-			: IGG (	ct (	CTG ·	CTG (	CTC	52
444 445 446	CAA		•	_					c c i	ATG (	GCC '						52
444 445 446 447 448 449	CAA		•	_					- c c :	ATG (	GCC '	rgg (	Ala 1				52
444 445 446 447 448 449 450		GAGG(	CAG (	- CGCT(	CTCG	GG A	CGTC	rcca	сс;	ATG ( Mst ) -19	GCC (	rgg ( Frp /	Ala 1	Lsu : -15	Lsu :	Lsu	
444 445 446 447 448 449 450	CTC	ACC	CTC	- CGCT(	CTCG(	G A	CGTC".	TCCA(	C C ;	ATG ( Mst ) -19 TCC	GCC 'Ala '	TGG ( Trp }	Ala 1 CAG	Lsu : -15 TCT	Lsu : GCC	Lsu CTG	52 100
444 445 446 447 448 449 450 451 452	CTC	ACC	CAG (CTC Leu	- CGCT(	CTCG(	G A	CGTC".	ACA	C C ;	ATG ( Mst ) -19 TCC	GCC 'Ala '	rgg ( Frp /	CAG Gln	Lsu : -15 TCT	Lsu : GCC	Lsu CTG	
444 445 446 447 448 449 450 451 452 453	CTC	ACC	CTC	- CGCT(	CTCG(	G A	CGTC".	TCCA(	C C ;	ATG ( Mst ) -19 TCC	GCC 'Ala '	TGG ( Trp }	Ala 1 CAG	Lsu : -15 TCT	Lsu : GCC	Lsu CTG	
444 445 446 447 448 449 450 451 452 453 454	CTC Leu	ACC Thr	CTC Leu -10	CTC Leu	CTCG( ACT Thr	CAG	GAC Asp	ACA Thr	GGG Gly	ATG ( Mst ) -19 TCC Ser	GCC Ala TGG	TGG ( Trp / GCC Ala	CAG Gln 1	Lsu : -15 TCT Ssr	GCC Ala	Lsu CTG Lsu	100
444 445 446 447 448 449 450 451 452 453 454 455	CTC Leu ACT	ACC Thr	CTC Leu -10	CTC Leu	ACT Thr	CAG Gln GTG	GAC Asp	ACA Thr -5	GGG Gly	ATG (Mst ) -19 TCC Ser	GCC Ala STGG Trp	GCC Ala	CAG Gln 1	Lsu : -15 TCT Ssr	GCC Ala	CTG Lsu ATC	
444 445 446 447 448 449 450 451 452 453 454 455	CTC Leu	ACC Thr	CTC Leu -10	CTC Leu	ACT Thr	CAG Gln GTG	GAC Asp	ACA Thr -5	GGG Gly	ATG (Mst ) -19 TCC Ser	GCC Ala STGG Trp	GCC Ala	CAG Gln 1	Lsu : -15 TCT Ssr	GCC Ala	CTG Lsu ATC	100
444 445 446 447 448 449 450 451 452 453 454 455 456	CTC Leu ACT Thr	ACC Thr	CTC Leu -10	CTC Leu	ACT Thr	CAG Gln GTG Val	GAC Asp	ACA Thr -5	GGG Gly	ATG (Mst ) -19 TCC Ser	GCC TGG Trp GGA Gly	GCC Ala	CAG Gln 1	Lsu : -15 TCT Ssr	GCC Ala	CTG Lsu ATC	100
444 445 446 447 448 449 450 451 452 453 454 455 456 457	CTC Leu ACT Thr	ACC Thr CAG	CTC Leu -10 CCT Pro	CTC Leu GCC Ala	ACT Thr TCC Ser	CAG Gln GTG Val	GAC Asp TCT Ser	ACA Thr -5 GGG	GGG Gly TCT Ssr	ATG (Mst ) -19 TCC Ser CCT Pro	TGG Trp GGA Gly	GCC Ala	CAG Gln 1 TCG Ssr	Lsu : -15 TCT Ssr ATC	GCC Ala ACC Thr	CTG Lsu ATC Ils 20	100
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460	CTC Leu ACT Thr 5	ACC Thr CAG Gln	CTC Leu -10 CCT Pro	CTC Leu GCC Ala	ACT Thr TCC Ser	CAG Gln GTG Val 10	GAC Asp TCT Ser	ACA Thr -5 GGG Gly	GGG Gly TCT Ssr	ATG (Mst ) -19  TCC Ser  CCT Pro	TGG Trp GGA Gly 15	GCC Ala	CAG Gln 1 TCG Ssr	Lsu : -15 TCT Ssr ATC Ils	GCC Ala ACC Thr	CTG Lsu ATC 11s 20	100 148
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 460 461	CTC Leu ACT Thr 5	ACC Thr CAG Gln	CTC Leu -10 CCT Pro	CTC Leu GCC Ala	ACT Thr TCC Ser	CAG Gln GTG Val 10	GAC Asp TCT Ser	ACA Thr -5 GGG Gly	GGG Gly TCT Ssr	ATG (Mst ) -19  TCC Ser  CCT Pro	TGG Trp GGA Gly 15	GCC Ala  CAG GIn	CAG Gln 1 TCG Ssr	Lsu : -15 TCT Ssr ATC Ils	GCC Ala ACC Thr	CTG Lsu ATC 11s 20	100 148
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 460 461 462	CTC Leu ACT Thr 5 TCC Ser	ACC Thr CAG Gln TGC Cys	CTC Leu -10 CCT Pro	CTC Leu GCC Ala GGA Gly	ACT Thr TCC Ser ACC Thr	CAG Gln GTG Val 10 AAC Asn	GAC Asp TCT Ser AAT Asn	ACA Thr -5 GGG Gly GAT Asp	GGG Gly TCT Ssr GTT Val	TCC Ser CCT Pro	TGG Trp GGA Gly 15 AGT Ssr	GCC Ala  CAG Gln  TAT Tyr	CAG Gln 1 TCG Ssr AAC	Lsu : -15 TCT Ssr ATC Ils CTT Lsu	GCC Ala  ACC Thr  GTC Val  35	CTG Lsu ATC Ils 20 TCC Ser	100 148 196
444 445 446 447 448 449 450 451 452 453 456 457 458 460 461 462 463	CTC Leu ACT Thr 5 TCC Ser	ACC Thr CAG Gln TGC Cys	CTC Leu -10 CCT Pro	CTC Leu GCC Ala GGA Gly	ACT Thr TCC Ser ACC Thr 25	CAG Gln GTG Val 10 AAC Asn	GAC Asp TCT Ser AAT Asn	ACA Thr -5 GGG Gly GAT Asp	GGG Gly TCT Ssr GTT Val	TCC Ser  CCT Pro  GGG G1y 30  CCC	GCC Ala TGG Trp GGA Gly 15 AGT Ssr	GCC Ala  CAG Gln  TAT Tyr	CAG Gln 1 TCG Ssr AAC Asn	Lsu : -15  TCT Ssr  ATC Ils  CTT Lsu  ATT	GCC Ala ACC Thr GTC Val 35	CTG Lsu ATC Ils 20 TCC Ser	100 148
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 461 462 463 464	CTC Leu ACT Thr 5 TCC Ser	ACC Thr CAG Gln TGC Cys	CTC Leu -10 CCT Pro	CTC Leu GCC Ala GGA Gly CAG	ACT Thr TCC Ser ACC Thr 25	CAG Gln GTG Val 10 AAC Asn	GAC Asp TCT Ser AAT Asn	ACA Thr -5 GGG Gly GAT Asp	GGG Gly TCT Ssr GTT Val	TCC Ser  CCT Pro  GGG G1y 30  CCC	GCC Ala TGG Trp GGA Gly 15 AGT Ssr	GCC Ala  CAG Gln  TAT Tyr	CAG Gln 1 TCG Ssr AAC Asn	Lsu : -15 TCT Ssr ATC Ils CTT Lsu ATT Ile	GCC Ala ACC Thr GTC Val 35	CTG Lsu ATC Ils 20 TCC Ser	100 148 196
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 461 462 463 464 465	CTC Leu ACT Thr 5 TCC Ser	ACC Thr CAG Gln TGC Cys	CTC Leu -10 CCT Pro	CTC Leu GCC Ala GGA Gly	ACT Thr TCC Ser ACC Thr 25	CAG Gln GTG Val 10 AAC Asn	GAC Asp TCT Ser AAT Asn	ACA Thr -5 GGG Gly GAT Asp	GGG Gly TCT Ssr GTT Val	TCC Ser  CCT Pro  GGG G1y 30  CCC	GCC Ala TGG Trp GGA Gly 15 AGT Ssr	GCC Ala  CAG Gln  TAT Tyr	CAG Gln 1 TCG Ssr AAC Asn	Lsu : -15  TCT Ssr  ATC Ils  CTT Lsu  ATT	GCC Ala ACC Thr GTC Val 35	CTG Lsu ATC Ils 20 TCC Ser	100 148 196
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 460 461 462 463 464 465 466	CTC Leu ACT Thr 5 TCC Ser	ACC Thr CAG Gln TGC Cys	CTC Leu -10 CCT Pro ACT Thr	CTC Leu GCC Ala GGA Gly CAG Gln 40	ACT Thr TCC Ser ACC Thr 25 CAC	CAG Gln GTG Val 10 AAC ABN	GAC Asp TCT Ser AAT Asn GGC Gly	ACA Thr -5 GGG Gly GAT Asp	GGG Gly TCT Ssr Val GCC Ala	ATG (Mst 7-19) TCC Ser CCT Pro GGG Gly 30 CCC Pro	TGG Trp GGA Gly 15 AGT Ssr	GCC Ala  CAG Gln  TAT Tyr  ATC	CAG Gln 1 TCG Ssr AAC Asn	Lsu -15 TCT Ssr ATC Ils CTT Lsu ATT Ile 50	GCC Ala ACC Thr GTC Val 35 TAT	CTG Lsu ATC Ils 20 TCC Ser GAG Glu	100 148 196 244
444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 461 462 463 464 465	CTC Leu ACT Thr 5 TCC Ser TGG Trp	ACC Thr CAG Gln TGC Cys TAC Tyr	CTC Leu -10 CCT Pro	CTC Leu GCC Ala GGA Gly CAG Gln 40 CGG	ACT Thr TCC Ser ACC Thr 25 CAC His	CAG Gln GTG Val 10 AAC ABN CCA Pro	GAC Asp TCT Ser AAT Asn GGC Gly	ACA Thr -5 GGG Gly GAT Asp AAA Lys	GGG Gly TCT Ssr Val GCC Ala 45	ATG (Mat 7)  TCC Ser  CCT Pro  GGG Gly 30  CCC Pro	GCC TGG TTCP GGA Gly 15 AGT SST AAA Lys	GCC Ala  CAG Gln  TAT Tyr	CAG Gln 1 TCG Ssr AAC Asn ATG Met	Lsu : -15 TCT Ssr ATC Ils CTT Lsu ATT Ile 50 GGC	GCC Ala  ACC Thr  GTC Val  35  TAT Tyr	CTG Lsu ATC 11s 20 TCC Ser GAG Glu	100 148 196

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469			55					60					65				
470 471	ጥርጥ	ccc	3 3 C	N CG	GCC	TCC	CTC	מ כי מ	ልጥር	ጥርጥ	GGG	CTC	CNG	CCT	GNG	GAC	340
472											Gly						340
473		70					75				•	80				•	
474																	
475 476											GGT						388
477	85	Ala	АБР	TÄT	τλτ	90	Сув	Ser	TÅT	Ala	95	SAT	τλτ	1111	Val	100	
478											-						
479											GGT						436
480	Phe	Gly	Gly	Gly		Lys	Leu	Thr	Val		Gly	Gln	Pro	Lys		Ala	
481 482					105					110					115		
483	CCC	TCG	GTC	ACT	CTG	TTC	CCG	ccc	TCC	TCT	GAG	GAG	CTT	CAA	GCC	AAC	484
484											Glu						
485				120					125					130			
486	330	~~~		ama	ama.	mam	ama		3.00	ara	mma	ma a	aaa	aa.	aaa	CEC	532
487 488											TTC Phe						332
489	-,,		135			O, D		140	502	1106		-1-	145	027			
490																	
491											GTC						580
492 493	Thr	Val 150	Ala	Trp	Lys	Ala	Asp 155	Ser	Ser	Pro	Val	Lys 160	Ala	GIY	Vai	GIu	
494		150					133					100					
495	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	AAG	TAC	GCG	GCC	AGC	AGC	628
496	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	Ala	Ser		
497	165					170					175					180	
498 499	тат	СТС	AGC	СТС	ACG	ССТ	GAG	CAG	TGG	AAG	TCC	CAC	AGA	AGC	TAC	AGC	676
500											Ser						0.0
501	•				185				•	190					195		
502																	
503 504											GAG Glu						724
505	Cys	GIII	VQI	200	nis	GIU	GLY	Ser	205	Val	GIG	пув	1111	210	AIG	PIU	
506									_								
507					TAG	GTTC:	CAA 2	ACCC:	rcac(	<b>c</b> c c	CCCC	ACGG	G AG	ACTA	GAGC		776
508 509	Thr	Glu	Cys 215	Ser													
510			213														
511	TGC	AGGA:	rcc (	CAGG	GAG	GG G	rctc:	CCT	c cci	ACCC	CAAG	GCA:	rcaa(	GCC (	CTTCT	CCCTG	836
512																	
513	CAC	rcaa:	raa 2	ACCC:	rcaa:	CA A	ATAT:	rctc	TT A	STCA	ATCA	CAA	AAAA	AAA 2	AAAA	AAAAA	896
514 515	AAA																902
516	AAA																
517																	
518	(2)	) IN	FORM	ATIOI	N FOI	RSE	O ID	NO:	12:								
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#### Patent Application US/07/952,640

521 522				(B)	TY	PE: a	: 23! amin	ac:	id	scid	3									
523 524				(D)	TO	POLO	GY: .	linea	ar											
525		(:	ii) 1	MOLE	CULE	TYP	E: p	rote	in											
526 527		(:	xi) :	SEQUI	ENCE	DES	CRIP:	TION	: SEC	) ID	NO:	12:								
528																_				
529 530	Met -19	Ala	Trp	Ala	Leu -15	Leu	Leu	Leu	Thr	Leu	Leu	Thr	Gln	Asp	Thr	Gly				
531	-19				-13					-10					-3					
532	Ser	$\mathtt{Trp}$	Ala	Gln	Ser	Als	Leu		Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser				
533				1				5					10							
534 535	Pro	Glv	Gln	Ser	Ile	Thr	Ile	Ser	Cvs	Thr	Glv	Thr	Aen	Asn	Agp	Val				
536		15					20		-1		1	25								
537		_		_		<b>_</b>		_					_		_					
538 539	GIÅ	Ser	Tyr	Asn	Leu	Val	Ser	Trp	Tyr	Gln	Gln 40	His	Pro	GIŸ	Lys	A1a 45				
540	30					3.7					10					13				
541	Pro	Lye	Ile	Met		Tyr	Glu	Val	Ser	Lye	Arg	Pro	Ser	Gly		Ser				
542					50					55					60					
543 544	Asn	Arg	Phe	Ser	Glv	Ser	Lvs	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile				
545		5		65	1				70			-		75						
546			_			<b></b> .				_	_	_		_		_				
547 548	Ser	GIĀ	Leu 80	Gln	Ala	GIU	Aep	61u 85	Ala	Aep	Tyr	Tyr	Cye 90	Сув	Ser	Tyr				
549			-					00					30							
550	Ala		Ser	Tyr	Thr	Val		Phe	Gly	Gly	Gly		Lys	Leu	Thr	Val				
551 552		95					100					105								
553	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser				
554	110					115					120					125				
555 556	Car	G1.	Gl.,	Leu	Gln.		Non.	Tara	λla	ሞኮታ	Leu	To I	<b>~</b>	Lau	Tla	Cor				
557	per	GIU	Giu	nea	130	A14	ven	ауы	TTD	135	Tea	Val	Cys	Пеп	140	Der				
558																				
559	Asp	Phe	Tyr	Pro	Gly	Ala	Val	Thr		Ala	Trp	Lys	Ala		Ser	Ser				
560 561				145					150					155						
562	Pro	Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn				
563			160					165					170							
564 565	len	Tare	Tarr	Ala	λla	Ser	Sor	ጥረታ	T.011	Ser	T.011	Thr	Pro	Glu	Gln	Trn				
566	acii	175	- X -	w <sub>T</sub> q	TTG	291	180	- 7 -	Ter	D-G-F	a.∓u	185		~	~	5				
567															_	=				
568 569	Lye 190	Ser	Hie	Arg	Ser	Tyr 195	Ser	Сув	Gln	Val	Thr 200	Hie	Glu	Gly	Ser	Thr 205				
570	T20					T33					<b>4</b> 00					200				
571	Val	Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu		Ser	,	-							
572					210					215		(2)	IN	FORM	OITA	Y FOR	SEQ	ID	NO:	13:
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573																		
574		(1)	) SE	_														
575					ENGT					3								
576			(1	B) T	YPE:	nuc.	leic	aci	1									
577			-	•	TRANI				h.									
578			(1	D) T(	OPOL	OGY:	line	ear										
579																		
580		(ii)	MOI	LECU	LE T	YPE:	CDN	A.										
581																		
582		(iii)	HY	POTH	ETIC	AL: I	OR											
583																		
584		(iv)	AN'	ri-Si	ENSE	: NO												
585		•-																
586																		
587		(ix)	) FE	ומוזיים	ਜ਼:•													
588		( 4-4-)			AME/I	ZEV.	CDS											
589			_		CAT:			221										
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59 <b>1</b>																		
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592		(X1	SE	SORM	ות אנ	ESCR.	TEAT	JN: i	SEQ.	וא עו	): 13	•						
593								<b></b>					~~		~	~~~		4.0
594			CAG		_													48
595	-	Ile	Gln	Met		GIn	Ser	Pro	Ser		Leu	Ser	Ala	ser		GTA		
596	1				5					10					15			
597																		
598			GTC															96
599	Asp	Arg	Val	Thr	Ile	Thr	Сув	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Tyr		
600				20					25					30				
601																		
602	TTA	AAT	TGG	TAT	CAA	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC		144
603	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile		
604			35	_			_	40	_				45					
605																		
606	TAT	GCT	GCA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	ACA	TCA	AGG	TTC	AGT	GGC		192
607			Ala															
608	-1-	50					55		2			60	3					
609																		
610	A CT	CCA	TCT	aaa	A C A	GAC	ጥጥር	ልሮሞ	מידים	אממ	<b>አ</b> ሞሮ	ACC	ACT	СТС	CAA	ССТ		240
611			Ser															2.0
612		_		_	1114	_		1111	100			DOL	561	204	0211	80		
613	65					, 0					,,,					- 00		
		C 3 E	TCT	<b>a</b> a.	3.00	mad	mad	mam	(13.3	as a	2 (18)	ma.c	3.00	3.00	CITIC!	አመረገ		288
614																		400
615	GIU	Asp	Ser	Ala		TYT	TYE	Cys	GIN		ser	Tyr	ser	Thr		TTe		
616					85					90					95			
617																		
618			GGC															321
619	Thr	Phe	Gly		Gly	Thr	Arg	Leu		Ile	Lys						•	
620				100					105									
621																		
622																		
623	(2)	INI	FORM	ATIO	V FO	R SE	QID	NO:	14:									
624																		

# Raw Sequence Listing

06/27/93 13:07:41 S5963.raw

625			(i)	SEQU	ENCE	CHAI	RACT	ERIS'	TICS:	:						
626				(A)	) LE	NGTH	: 10	7 am	ino a	acid	8					
627				(B)	TY:	PE:	amin	0 sc:	id							
628				(D	TO:	POLO	GY: :	lins	ar							
629																
630		(:	ii) :	MOLE	CULE	TYP	E: p:	rots	in							
631		•					•									
632		(:	xi)	SEQU	ENCE	DES	CRIP'	TION	: SEC	O ID	NO:	14:				
633		•							,							
634	Asp	Ils	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Sar	Ala	Ser	Val	Glv
635	1				5					10					15	
636					_											
637	Asp	Arq	Val	Thr	Ile	Thr	Cvs	Ara	Ala	Ssr	Gln	Sar	Ils	Sar	Asn	Tvr
638		5		20			-,, -	3	25					30		
639														-		
640	Leu	Asn	Tro	Tyr	Gln	Gln	Lvs	Pro	Glv	Lvs	Ala	Pro	Lvs	Leu	Leu	Ile
641			35	-3-			-2-	40	2	-2-			45			
642																
643	Tvr	Ala	Als	Ssr	Ser	Lsu	Gln	Ser	Glv	Val	Thr	Sar	Ara	Phs	Sar	Glv
644	-3-	50					55		<b></b> 2			60	9	- 110		
645												•				
646	Sar	Glv	Ser	Gly	Thr	Asp	Phe	Thr	Len	Thr	Tle	Ser	Ser	T <sub>1</sub> e11	Gln	Pro
647	65	1		0-2		70					75					80
648						. •					, ,					•
649	Glu	Asp	Sar	Ala	Thr	Tvr	Tvr	Cvs	Gln	Gln	Sar	Tvr	Sar	Thr	Lsu	Ila
650					85	-1-	-1-	-,, -		90		-1-			95	
651					-											
652	Thr	Phe	Glv	Gln	Glv	Thr	Ara	Leu	Glu	Ile	Lvs					
653				100	4		5		105		-2-					
654																
655	(2)	IN	FORM	ATIO	1 FO	R SEC	O ID	NO:	15:							
656	`-,					,	<b>.</b>									
657		(i)	) SE	QUEN	CE CI	HARA	CTER:	ISTI	CS:							
658		•		A) LI						3		*				
659				B) T				_		_						
660			-	c) s:												
661			Ò	D) T(	POL	OGY:	lina	ssr	_							
662			•													
663		(ii)	MO	LECUI	LE T	YPE:	cDN	A.								
664		•														
665		(iii)	HY	POTH	ETIC	AL: 1	10									
666			<i>*</i>													
667		(iv	AN	TI-SI	ENSE	: NO										
668		•														
669																
670		(ix)	FE	ATURI	3:											
671				A) N		KEY:	CDS									
672				B) L	-			324								
673			•	,,				_ =								
674																
675		(xi	) SE	QUEN	CE DI	ESCR:	[PTIC	ON:	SEO I	D NO	15:15	:				
676									~ -							

# Raw Sequence Listing

06/27/93 13:07:48 S5963.raw

677 678 679		ATT Ile													Val		48
680	_				3					10					15		
681	GAC	AGA	CTC	ACC	ልሞሮ	ACC	TCC	» CC	CCA	аст	CAG	ccc	አጥጥ	N.C.C	СУП	ጥአጥ	96
682		Arg															20
683		5		20			0,2	9	25		<b></b>	1		30		-3-	
684														-			
685	TTA	AGT	TGG	TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	GAG	CTC	CTG	ATC	144
686		Ser															
687			35	-			-	40	_	-			45				
688																	
689	TAT	GCT	GCT	TCC	AGT	TTG	CAA	AGT	GGG	ATT	CCC	TCT	CGG	TTC	AGC	GGC	192
690	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
691		50					55					60					
692																	
693		GGA															240
694		Gly	Ser	Gly-	Thr		Phe	Thr	Leu	Thr		Ser	Ser	Leu	Gln	Pro	
695	65					70					75					80	
696	~	~															
697		GAT														_	288
698	GIU	Asp	ser	Ala		TAL	TYT	Сув	GII		Inr	TAL	ser	Авр		TYT	
699 700					85					90					95		
701	አርጥ	TTT	ccc	CAG	ccc	N.C.C	***	CTC	GNC	አጥሮ	***	CCA					324
702		Phe															324
703	-	* 110	<b>-1</b>	100	O-y		-y 5	vul	105	110	Dy G	nr 9					
704																	
705																	
706	(2)	INI	ORM	TION	I FOI	SEC	ID	NO:	L6:								
707																	
708			(i) 8	EQUE	ENCE	CHAI	RACTE	RIST	CICS:	:							
709				(A)	LE	GTH:	: 108	am:	lno a	acida	3						
710				(B)	TYI	?E: 8	amino	ac	id								
711				(D)	TOI	OLOC	Y: ]	Linea	ar								
712																	
713		( :	Li) 1	OLEC	CULE	TYPE	e: pr	ote	ln								
714																	
715		(3	ci) S	EQUE	ENCE	DESC	RIPI	CION:	SEÇ	) ID	NO:	L6:					
716				_			_	_	_		_	_		_			
717	_	Ile	GIN	Leu	_	GIN	Ser	Pro	ser	_	Leu	Ser	Ala	Ser		GTĀ	
718	1				5					10					15		
719 720	. 7	λ	77 m 7	<b>77.</b> ~	T1 ~	77 h	~-~	7 m-	27-	d ~~	<b>@1</b> =	<b>G</b> 1	T1-	d ~ ~	7 e-	The pass	•
720 721	Asp	wrg	AGT	20	тте	T 111.	CYB	wrg	A14 25	Ser	GIII	стХ	TTO	30	дам	TÄL	
722				20					49					30			
723	Len	Ser	Tro	Tvr	Gl n	Gln	I.vs	Pro	GI v	Lva	Ala	Pro	Glu	Len	Len	Ile	
724	204	291	35	~ y _			-y	40	G L y	-y a	n-a		45	264	250		
725		•	-														
726	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Glv	Ile	Pro	Ser	Aro	Phe	Ser	Glv	
727	- 2 -	50			~		55	~				60	3			2	
728							-										

# Raw Sequence Listing

06/27/93 13:07:54 S5963.raw

729 730 731	Ser 65	Gly	Ser	Gly	Thr	Aep 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80	
732 733 734	Glu	Aep	Ser	Ala	Val 85	Tyr	Tyr	Суе	Gln	Hie 90	Thr	Tyr	Ser	Aep	Pro 95	Tyr	
735 736 737	Ser	Phe	Gly	Gln 100	Gly	Thr	Lye	Val	Asp 105	Ile	Lys	Arg					
738 739	(2)	INI	FORM	ATIOI	I FOI	SE(	O ID	NO:	L7:								
740		(i)	SE	QUEN	CE CE	IARA	CTER:	STI	CS:								
741			(2	A) LI	engti	1: 32	24 ba	ase p	pair	3							
742				-			Leic										
743				-			ESS:		1								
744 745			(1	)) T(	DEOPO	JGY:	line	ear									
746		(11)	MOI	LECUI	E T	PE:	cDN	<b>A</b>									
747		,,						-									
748		(iii)	HYI	POTHI	ETIC	AL: 1	10										
749																	
750		(iv)	AN.	ri-Si	ENSE	: ио											
751																	
752 753		12	1 12121	, entro	a .												
754		(IX,	) FE2	Alori		rv.	CDG										
755							1	324									
756			``	,													
757																	
758		(xi)	SE	QUEN	CE DE	SCR	[PTI	on: S	SEQ :	D NO	17:	:					
759																	
760			CAG														48
761	-	Ile	Gln	Leu		Gln	Ser	Pro	Ser		Leu	Ser	Ala	Ser		Gly	
762	1				5					10					15		
763 764	CAC	a ca	GTC	» cc	አጥ <b>ሮ</b>	ልሮጥ	тас	ccc	CCA	ACT	CAG	ccc	<b>Δ ΤΡΤ</b> Ι	ACC	ልረጥ	таπ	96
765			Val														50
766		9		20			- I	9	25		V	,		30		-7-	
767																	
768	TTA	AGT	TGG	TAT	CAG	CAG	AAA	CÇA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	144
769							_	_		T	Ala	73	<b>T</b>	T		TIA	
770		Ser	Trp	Tyr	Gln	GIn	гЛа	Pro	GTĀ	гАв	WT a	Pro	гЛа	ren	Leu	TTA	
		Ser	Trp 35	Tyr	Gln	GIn	гув	Pro 40	GTA	гув	ALG	Pro	ьув 45	Ten	ren	116	
771	Leu		35	- -				40	_	_			45				1.00
772	Leu	TAT	35 GCA	AAC	AGT	TTG	GCA	40 AGT	GGG	GTC	CCA	TCA	45 AGG	TTC	AGC	GGC	192
772 773	Leu	TAT Tyr	35	AAC	AGT	TTG	GCA Ala	40 AGT	GGG	GTC	CCA	TCA Ser	45 AGG	TTC	AGC	GGC	192
772 773 774	Leu	TAT	35 GCA	AAC	AGT	TTG	GCA	40 AGT	GGG	GTC	CCA	TCA	45 AGG	TTC	AGC	GGC	192
772 773	Leu TAT Tyr	TAT Tyr 50	35 GCA	AAC Asn	AGT Ser	TTG Leu	GCA Ala 55	40 AGT Ser	GGG Gly	GTC Val	CCA Pro	TCA Ser 60	45 AGG Arg	TTC Phe	AGC Ser	GGC Gly	192 240
772 773 774 775	TAT Tyr AGT	TAT Tyr 50 GGA	35 GCA Ala	AAC Asn	AGT Ser ACA	TTG Leu GAA	GCA Ala 55 TTC	40 AGT Ser	GGG Gly CTC	GTC Val	CCA Pro	TCA Ser 60 AGC	AGG Arg	TTC Phe CTG	AGC Ser CAG	GGC Gly CCT	
772 773 774 775 776	TAT Tyr AGT	TAT Tyr 50 GGA	35 GCA Ala TCT	AAC Asn	AGT Ser ACA	TTG Leu GAA	GCA Ala 55 TTC	40 AGT Ser	GGG Gly CTC	GTC Val	CCA Pro	TCA Ser 60 AGC	AGG Arg	TTC Phe CTG	AGC Ser CAG	GGC Gly CCT	
772 773 774 775 776 777	TAT Tyr AGT Ser 65	TAT Tyr 50 GGA Gly	35 GCA Ala TCT	AAC Asn GGG Gly	AGT Ser ACA Thr	TTG Leu GAA Glu 70	GCA Ala 55 TTC Phe	AGT Ser ACT Thr	GGG Gly CTC Leu	GTC Val ACC Thr	CCA Pro ATC Ile 75	TCA Ser 60 AGC Ser	AGG Arg AGC Ser	TTC Phe CTG Leu	AGC Ser CAG Gln	GGC Gly CCT Pro 80	

#### Raw Sequence Listing

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781 782 783	G1u	Asp	Ser	Ala	Thr 85	Tyr	Tyr	Сув	Gly	Gln 90	Gly	Asn	Ser	Tyr	Pro 95	Leu	
784 785 786				GGA Gly 100													324
787 788 789	(2)	) IN	FORM	ATIO	N FO	R SE	Q ID	NO:						•			
790 791 792			(i)	SEQUI						: acid	9						
793 794 795				(D)	TO	POLO	amino 3Y: :	Line	ar								
796 797 798				MOLE SEQUI			_			Q ID	NO:	18:					
799 800 801 802	Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15	Gly	
803 804 805	Asp	Arg	Va1	Thr 20	Ile	Thr	Сув	Arg	Ala 25	Ser	Gln	Gly	Ile	Ser 30	Thr	Tyr	
806 807 808	Leu	Ser	Trp 35	Tyr	G1n	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	Leu	Leu	Ile	
809 810 811		50		Asn			55					60				_	
812 813 814	65	Ī		Gly		70					75					80	
815 816 817				Ala	85					90			Ser	Tyr	Pro 95	Leu	
818 819 820 821			_	Gly 100 ATION					105	116	тАв	Arg					
822 823 824	(2)		) SE	QUEN( A) Li	CE CI	HARA	TER:	ISTIC	cs:	~							
825 826 827			(1	B) T3 C) S3 D) T(	PE: PRANI	nuc: DEDNI	Leic ESS:	acio	E	<b>.</b>							
828 829 830		(ii	) мо:	LECUI	LE T	YPE:	cDN	A									
831 832		(iii	) HY:	ротні	ETIC	AL: 1	<b>10</b>										

#### Raw Sequence Listing

06/27/93 13:08:08 S5963.raw

833 834		(iv	) AN	ri-si	ense	: NO											
835					-												
836 837		(1X	) FE			PTOSE .	ana										
838				A) NZ B) L(				324									
839			١.	5/ <u>I</u> I	JURI.	ION.	<b>+••</b>	744									
840																	
841		(xi	) SE	OUEN	CE DI	ESCR	TPTT	on:	SEO '	TD N	0:19	•					
842		,		<b>,</b>	J				×.								
843	GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCT	CAG	TCT	GCA	TCT	GTA	GGA	48
844	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Gln	Ser	Ala	Ser	Val	Gly	
845	1				5					10	4				15	_	
846																	
847	GAC	AGA	GTG	ACC	ATT	ACT	TGC	CAG	GCG	AGT	CAA	AGC	CTT	AGC	AAT	TAT	96
848	Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ala	Ser	Gln	Ser	Leu	Ser	Asn	$\mathtt{Tyr}$	
849				20					25					30			
850																	
851			TGG														144
852	теп	Asn	Trp	Tyr	GIN	GIN	ьys		GIĀ	Lys	Ile	Pro		Leu	Leu	He	
853 854			35					40					45				
855	ጥአጥ	N.C.C	GCA	TOC	N CITT	ጥጥረ	C2 2	አረጥ	000	እጥጠ	aaa	møm	aaa	mmæ	200	000	192
856			Ala			_	-										192
857	-1-	50		Der	061	266	55	~ CI	CIY			60	n- 9	1110	DOL	Gry	
858												•					
859	AGT	GGA	TCT	GGG	ACG	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAG	CCT	240
860			Ser														
861	65	_		_		70					75					80	
862																	
863	GAA	GAT	TTŢ	GCC	ACT	TAT	TAC	TGT	CAG	CAT	AAT	TAT	GGT	ACC	CCT	CTC	288
864	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Сув	Gln	His	Asn	$\mathbf{T}\mathbf{y}\mathbf{r}$	Gly	Thr	Pro	Leu	
865					85					90					95		
866																	
867			GGC														324
868 869	Thr	Pne	Gly	100	GIĀ	Thr	гля	val		TTÉ	ьуѕ	Arg					
870				100					105								
871																	
872	(2)	TN	FORM	ATTON	v FOI	R SE	מד כ	NO:	20:								
873	,-,						£										
874			(i) s	SEQUE	ENCE	CHAI	RACTI	ERIS:	rics:	:							
875								am:			3						
876				(B)	TY	PE: 8	amino	ac:	id								
877				(D)	TO	OTO	3Y: :	linea	ar								
878																	
879		(:	Li) 1	MOLE	CULE	TYPI	E: pi	rote:	ln								
880																	
881		(2	ci) S	SEQUE	ENCE	DES	CRIP:	LION	: SE(	2 ID	NO:2	20:					
882	7	<b>71.</b>	<b>~</b> 11	T 4	M1	<b>41</b>	O	Desc	O		<b>a</b> 1	Cl c	27	0	77 c 7	<i>α</i> 1	
883 884	Asp 1	тт <del>е</del>	Gln	тéп	Thr 5	'GTU	ser	KIO	ser	_	GIN	Ser	ATS	ser	Va1	GTA	
004					5					10					13		

#### Raw Sequence Listing

06/27/93 13:08:15 S5963.raw

885																		
886	Asp	Arg	Val	Thr	Ile	Thr	Сув	G1n	Ala	Ser	Gln	Ser	Leu	Ser	Asn	Tyr		
887				20					25					30				
888												•						
889	Leu	Asn	Trp	Tyr	G1n	G1n	Lys	Pro	G1y	Lys	Ile	Pro	Lys	Lsu	Lsu	Ile		
890			35					40					45					
891																		
892	Tyr	Arg	Ala	Ser	Ser	Leu	Gln	Ser	G1y	Ile	Pro	Ser	Arg	Phs	Ser	G1y		
893		50					55					60						
894																		
895	Ser	G1y	Ser	Gly	Thr	Asp	Phs	Thr	Lsu	Thr	I1s	Ser	Ser	Lsu	Gln	Pro		
896	65					70					75					80		
897																		
898	G1u	Asp	Phs	Ala	Thr	Tyr	Tyr	Сув	G1n	His	Asn	Tyr	Gly	Thr	Pro	Lsu		
899		-			85	-	_	_		90		Ī	_		95			
900																		
901	Thr	Phs	G1y	G1y	G1y	Thr	Lys	Va1	G1u	Ils	Lys	Arg						
902			-	100	-		-		105		-	_						
903																		
904	(2)	INE	ORM	ATIO	1 FOI	R SE	QID	NO:	21:									
905						•	-											
906		(i)	SEC	OUEN	CE CI	HARA	TER.	ISTIC	CS :									
907		` '		-				ase p		8								
908								acio										
909			((	c) s:	rani	DEDNI	zss:	botl	1									
910			(1	D) T(	POL	OGY:	line	ear										
911			•															
912		(ii)	MOI	LECUI	LE T	YPE:	DNA	(gsı	nomi	c)								
913		••																
914																		
915		(ix)	FE	ATUR	Ξ:													
916			(2	A) N2	AME/I	KEY:	CDS											
917				3) L(				324										
918			·	•														
919		(xi)	SEC	OUEN	CE DI	ESCR:	[PTI	on: S	SEO :	ID NO	0:21	:						
920				-					_									
921	GAC	ATTC	AGC 1	rgac(	CAG	rc To	CAC	CTC	CTC	GCCC	GTCA	GTC:	TTGG	AGA (	GTCG	CCTCC	?	60
922																		
923	ATC:	CCT	ו ממו	INNN	INNNI	IN NE	NNNN	MNNN	NN I	INNN	NNNN	NNN	וממממ	NNN I	INNN	MININN	ī	120
924																		
925	NNNI	MMM	INN I	NNNN	NNNN	NN NI	NNNN	MNNN	NN I	NNNN	NNNN	NNN	NNNN	NNN 1	NTC	CCAGAC	:	180
926																		
927	AGG'	TCAC	CTG (	GCAG'	rggg:	rc ac	GCA	CTGA:	r TT	CACA	CTGA	AAA:	rcag(	CAG 2	AGTG	GAGGCT	•	240
928																		
929	GAG	GATGI	TG (	GGGT:	TAT:	TA C	rgca:	rgca.	A GC	CTT	CGGT	CTC	CTTG	GAC (	GTTC	GCCAA		300
930						-				_								
931	GGG	ACCAZ	AGG :	rgga:	AATC	AG A	CGA											324
932																		
933																		
934	(2)	INI	ORM	ATIO	N FOI	R SEG	Q ID	NO:	22:									
935	•						-											
936		(i)	SEC	DUEN	CE C	HARA	CTER	ISTIC	cs:									

#### Raw Sequence Listing

06/27/93 13:08:21 \$5963.raw

937 938 939			) LEI ) TYI ) TOI	PE: 8	amino		id	acid	S							
940 941	(11)	MOL	ECULI	2 TVI	P12 - 1	arot	ain.									
942	(11)	11021				p-00.										
943	(xi)	SEQ	UENCI	Z DE	SCRI	PTIO	N: SI	EQ II	ОИО	:22:						
944 945	дед	I1e	G1n	Leu	Thr	G1n	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Glv
946	1				5					10					15	2
947	e4				-1-	m1	77	77	2m					<b>47</b>		
948 949	Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xa															
950	Xaa															
951	Xaa															
952 953	35 40 45															
954	35 40 45  Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Xaa Xaa Thr Xaa															Xaa
955		50					55					60				
956 957	Vaa	Yes	Xaa	Yaa	V	V	Vaa	Vaa	Yaa	Larg	V	Vaa	7 ~~	17-5 7	GI.	71.0
958	65	Aaa	Add	naa	naa	70	Add	Aaa	Aaa	пув	75	Add	ALG	Val	GIU	80
959																
960	Xaa	Xaa	Val	Gly		Xaa	Xaa	Xaa	Met		Ala	Leu	Arg	Ser		Trp
961 962					85					90					95	
963	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lye	Va1	Xaa	Xaa	Arg	Arg				
964				100					105							
965 966																
967	(2) INF	ORMA!	TION	FOR	SEQ	ID I	NO: 23	3:								
968	(2)	a Ho					3m <b>- ~</b>	٠.								
969 970	(1)		UENCI ) LEI													
971			) TYI													
972			) STI													
973 974		(D)	) TOI	OTO:	3Y: :	line	ar									
975	(ii)	MOL	ECULI	Z TYI	PE: (	cDNA										
976																
977	(iii)	HYP	OTHE	[ICA]	L: NO	)										
978 979	(iv)	ANT	I-SEI	NSE:	NO											
980	(2.7															
981																
982 983	(1x)		TURE: ) NAI			פחים										
984			) LO				24									
985																
986	/41	anc.		3 P.E.	age z	DM 7 ^ '	NT	PA T	n 174							
987 988	(X1)	2EQ	UENC	s DE:	CRL	LTO!	N: 51	₽Õ TI	יטא ט	43:						
<b>-</b>																

#### Raw Sequence Listing

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989	GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCT	TCC	CTG	TCT	GCA	TCG	GTA	GGA	48
990	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Va1	Gly	
991	1				5					10					15		
992																	
993					ATC												96
994	Asp	Arg	Val		Ile	Thr	Cys	Arg		Ser	Gln	Gly	Ile		Asp	Tyr	
995				20					25					30			
996	mma	3 am	maa	ma m	~~	~~			-		aam	aam		ama	ama	3 ma	244
99 <b>7</b> 998					CAG											_	144
999	ren	Ser	35	ıyr	G1n	GIII	гув	40	GIY	ьув	AIA	PIO	ьув 45	Leu	Leu	TIE	
1000			33					40					40				
1001	TAT	GCT	GCA	TCC	AGT	ጥጥር	CAA	ACT	ccc	GTC	CCA	TCA	ACC	ጥጥሮ	AGC	GGC	192
1002					Ser												1,2
1003	-1-	50					55		<b>1</b>			60	5			<b>-1</b>	
1004																	
1005	AGT	GGA	TCT	GGG	ACA	GAA	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAA	CCT	240
1006	Ser	G1y	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
1007	65	_		_		70					75					80	
1008																	
1009	GAA	GAT	TTT	GCA	ACT	TAT	TAC	TGT	CTA	CAG	GGT	TAT	GGT	ACC	CCG	TAC	288
1010	G1u	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly	Tyr	Gly	Thr	Pro	Tyr	
1011					85					90					95		
1012																	
1013					GGG												324
1014	Ser	Phe	Gly		Gly	Thr	Lys	Val		Ile	Lys	Arg					
1015				100					105								
1016																	
1017	(0)																
1018 1019	(2)	TN	TORM	ATTOI	4 FOI	K SE(	S ID	NO:	44:								
1019			(4) (	FOIT	ENCE	CHAI	מייים א	PDTC	rTCC.								
1021			(1)	_	LEI						27						
1022					TYI					<u>.</u>	•						
1023					TOI												
1024				()													
1025		(:	ii) 1	MOLE	CULE	TYPE	: E	rote	ln								
1026		•	•				-										
1027		(3	ci) 8	SEQUI	ENCE	DESC	CRIP:	TION:	SE(	QI Ç	NO:2	24:					
1028																	
1029	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	A1a	Ser	Vel	Gly	
1030	1				5					10					15		
1031																	
1032	Asp	Arg	Val		Ile	Thr	Cys	Arg		Ser	Gln	Gly	Ile		Asp	Tyr	
1033				20					25					30			
1034		_					_	_		_	_ •-	_		_	_		
1035	T	Car	TTT	Tvr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
	Leu	SOL		-1-													
1036	Leu	261	35	-1-				40					45				
1037			35				<b>a</b> •	_	<b>~</b> ?	1		<b>5</b> .		<b>5</b> 1 -	<b>5</b>	<b>~</b> 3	
1037 1038		Ala	35		Ser	Leu		_	Gly	Val	Pro			Phe	Ser	Gly	
1037			35			Leu	<b>G1n</b> 55	_	Gly	Val	Pro	Ser 60		Phe	Ser	Gly	

# Raw Sequence Listing

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1041																	
	Ser (	G1y	Ser	G1y	Thr		Phe	Thr	Leu	Thr		Ser	Ser	Leu	G1n		
1042 1043	65					70					75					80	
1043	Glu 2	7	Pho	212	The	The	There	Care	Lou	G1 m	G1 **	T'	C1**	The	Bro	There	
1045	GIU 2	qan	FIIG	AIG	85	TYL	TYL	Cys	Leu	90	GIY	TYL	GTÅ	TILL	95	IYL	
1046					05					50					,,		
1047	Ser I	Phe	G1v	G1n	G1v	Thr	Lvs	Va1	G1u	Ile	Lvs	Arg					
1048			3	100	4		-3 -		105		-3	5					
1049																	
1050	(2)	INE	ORM	ATIO	I FOI	R SE	QI C	NO:	25:								
1051																	
1052		(i)	SE	QUEN	CE CE	IARA(	CTER:	ISTI	CS:								
1053			(2	7) L1	engti	1: 3:	24 ba	ase j	pair	3							
1054			-	•	YPE:												
1055				-	rani				n								
1056			(1	) T	POL	GY:	1ine	ear									
1057																	
1058		(ii)	MOI	LECUI	LE T	PE:	CDN2	A.									
1059																	
1060	(:	111)	HYI	POTH	ETIC	YP: I	ON										
1061 1062		(	3 370		3 <b>1</b> 0 m	NTO.											
1062		(17)	AN.	TT-21	ENSE	: NO											
1063																	
1065		(i~)	RT2	ATURI	7.												
1066		( 42,			AME/I	CEY:	CDS										
1067					CAT			324									
			٠,-	-, -													
1068																	
1068 1069																	
1069		(xi)	SE(	OUENO	CE DI	sscr:	IPTI(	ON: 8	SEO I	ED NO	0:25:	:					
		(xi)	SEÇ	)UEN	CE DI	3SCR	[PTI(	ON: A	SEQ I	ED NO	25:						
1069 1070	GAC 1		-	_					_				GCA	TCT	GTG	GGA	48
1069 1070 1071		ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT					48
1069 1070 1071 1072	GAC I	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT					48
1069 1070 1071 1072 1073	GAC A	ATT	CAG	CTG	ACC Thr	CAG	TCT	CCA	TCC	TCC Ser	CTG	TCT			Vs1		48
1069 1070 1071 1072 1073 1074 1075	GAC A	ATT Ile	CAG G1n GTC	CTG Leu	ACC Thr 5	CAG G1n ACT	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu CAG	TCT Ser	A1a ATT	Ser AGC	Vs1 15 AAT	Gly AAT	<b>48</b> 96
1069 1070 1071 1072 1073 1074 1075 1076	GAC Asp 1	ATT Ile	CAG G1n GTC	CTG Leu ACC Thr	ACC Thr 5	CAG G1n ACT	TCT Ser	CCA Pro	TCC Ser GCA Ala	TCC Ser 10	CTG Leu CAG	TCT Ser	A1a ATT	Ser AGC Ser	Vs1 15 AAT	Gly AAT	
1069 1070 1071 1072 1073 1074 1075 1076 1077	GAC A	ATT Ile	CAG G1n GTC	CTG Leu ACC	ACC Thr 5	CAG G1n ACT	TCT Ser	CCA Pro	TCC Ser	TCC Ser 10	CTG Leu CAG	TCT Ser	A1a ATT	Ser AGC	Vs1 15 AAT	Gly AAT	
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078	GAC A	ATT Ile ACA Ihr	CAG G1n GTC Va1	CTG Leu ACC Thr	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGT Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GAC Asp	A1a ATT I1e	AGC Ser 30	Vs1 15 AAT Asn	Gly AAT Asn	96
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080	GAC A Asp T	ATT Ile ACA Thr	CAG Gln GTC Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGT Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GAC Asp	A1a ATT I1e	AGC Ser 30	Vs1 15 AAT Asn	Gly AAT Asn	
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081	GAC A	ATT Ile ACA Thr	CAG Gln GTC Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGT Cys	CCA Pro CGG Arg CCA Pro	TCC Ser GCA Ala 25 GGG	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GAC Asp	ATT Ile AAG Lys	AGC Ser 30	Vs1 15 AAT Asn	Gly AAT Asn	96
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082	GAC A Asp T	ATT Ile ACA Thr	CAG Gln GTC Val	CTG Leu ACC Thr 20	ACC Thr 5 ATC Ile	CAG Gln ACT Thr	TCT Ser TGT Cys	CCA Pro CGG Arg	TCC Ser GCA Ala 25 GGG	TCC Ser 10 AGT Ser	CTG Leu CAG Gln	TCT Ser GAC Asp	A1a ATT I1e	AGC Ser 30	Vs1 15 AAT Asn	Gly AAT Asn	96
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083	GAC AASP TTA CLeu N	ATT I1e ACA Thr GTC Val	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGT Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GAC Asp CCT Pro	ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Vs1 15 AAT Asn CTG Leu	Gly AAT Asn ATC	96 144
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084	GAC AASP TTA CLEU TAT C	ATT Ile ACA Thr GTC Val	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT TYr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGT Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GAC Asp CCT Pro	ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Vs1 15 AAT Asn CTG Leu	Gly AAT Asn ATC Ile	96
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085	GAC AASP TTA CLeu N	ATT Ile ACA Thr GTC Val	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT TYr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGT Cys AAA Lys CAA Gln	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GAC Asp CCT Pro	ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Vs1 15 AAT Asn CTG Leu	Gly AAT Asn ATC Ile	96 144
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086	GAC AASP TTA CLEU TAT C	ATT Ile ACA Thr GTC Val	CAG Gln GTC Val TGG Trp 35	CTG Leu ACC Thr 20 TAT TYr	ACC Thr 5 ATC Ile CAG Gln	CAG Gln ACT Thr CAG Gln	TCT Ser TGT Cys AAA Lys	CCA Pro CGG Arg CCA Pro 40	TCC Ser GCA Ala 25 GGG Gly	TCC Ser 10 AGT Ser AAA Lys	CTG Leu CAG Gln GCC Ala	TCT Ser GAC Asp CCT Pro	ATT Ile AAG Lys 45	AGC Ser 30 CTC Leu	Vs1 15 AAT Asn CTG Leu	Gly AAT Asn ATC Ile	96 144
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087	GAC ASP TATA (Leu Y	ACA Thr GTC Val	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr	ACC Thr 5 ATC Ile CAG Gln AGA Arg	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGT Cys AAA Lys CAA G1n 55	CCA Pro CGG Arg CCA Pro 40 GAT Asp	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG G1n GCC A1a CCA Pro	TCT Ser GAC Asp CCT Pro	ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Vs1 15 AAT Asn CTG Leu AGC Ser	AAT ASN ATC Ile GGC Gly	96 144 192
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088	GAC ASP TATA CLEU NATATA CAGT CAGT	ACA Thr GTC Val GCT Ala 50	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr TCC Ser	ACC Thr 5 ATC Ile CAG Gln AGA Arg	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGT Cys AAA Lys CAA G1n 55	CCA Pro CGG Arg CCA Pro 40 GAT Asp	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG G1n GCC A1a CCA Pro	TCT Ser GAC Asp CCT Pro TCA Ser 60	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Vs1 15 AAT Asn CTG Leu AGC Ser	AAT ASN ATC 11e GGC G1y GCT	96 144
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088	GAC AASP TATA (Leu Y	ACA Thr GTC Val GCT Ala 50	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr TCC Ser	ACC Thr 5 ATC Ile CAG Gln AGA Arg	CAG Gln ACT Thr CAG Gln TTG Leu GAT Asp	TCT Ser TGT Cys AAA Lys CAA G1n 55	CCA Pro CGG Arg CCA Pro 40 GAT Asp	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GAC Asp CCT Pro TCA Ser 60	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Vs1 15 AAT Asn CTG Leu AGC Ser	AAT ASN ATC Ile GGC Gly GCT Ala	96 144 192
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088	GAC ASP TATA CLEU NATATA CAGT CAGT	ACA Thr GTC Val GCT Ala 50	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr TCC Ser	ACC Thr 5 ATC Ile CAG Gln AGA Arg	CAG Gln ACT Thr CAG Gln TTG Leu	TCT Ser TGT Cys AAA Lys CAA G1n 55	CCA Pro CGG Arg CCA Pro 40 GAT Asp	TCC Ser GCA Ala 25 GGG Gly GGG Gly	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG G1n GCC A1a CCA Pro	TCT Ser GAC Asp CCT Pro TCA Ser 60	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Vs1 15 AAT Asn CTG Leu AGC Ser	AAT ASN ATC 11e GGC G1y GCT	96 144 192
1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088	GAC AASP TATA (Leu Y	ATT Ile ACA Thr GTC Val GGT A1a 50 GGG GGY	CAG Gln GTC Val TGG Trp 35 GCA Ala	CTG Leu ACC Thr 20 TAT Tyr TCC ser	ACC Thr 5 ATC Ile CAG Gln AGA Arg	CAG Gln ACT Thr CAG Gln TTG Leu GAT Asp	TCT Ser TGT Cys AAA Lys CAA Gln 55 TTC Phe	CCA Pro CGG Arg CCA Pro 40 GAT Asp	TCC Ser GCA Ala 25 GGG Gly GGG Gly CTC Leu	TCC Ser 10 AGT Ser AAA Lys GTC Val	CTG Leu CAG Gln GCC Ala CCA Pro	TCT Ser GAC Asp CCT Pro TCA Ser 60 AAT Asn	Ala ATT Ile AAG Lys 45 AGG Arg	AGC Ser 30 CTC Leu TTC Phe	Vs1 15 AAT Asn CTG Leu AGC Ser GAA Glu	AAT ASN ATC Ile GGC Gly GCT Ala 80	96 144 192

# Raw Sequence Listing

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1093 1094	Asp As	o Ala	Ala	Asp 85	Tyr	Tyr	Сув	Leu	Gln 90	Thr	Lys	Ser	Ser	Pro 95	Arg	
1095	3.00 mm	~ ~~~	~	~~~			ama	~			~~~					204
1096	ACG TT															324
1097	Thr Ph	e GIY		GIY	Thr	гЛя	val		TTG	гÃ8	Arg					
1098			100					105								
1099																
1100	(0) -		. m = 0:				***									
1101	(2) I	NFORM	ATTO	N FOI	K SE	î TD	NO:	26:								
1102		(1)	a = 0 = T		<i></i>											
1103		(1)	SEQUI													
1104							8 am		aclo	3						
1105							o ac				·					
1106			(D	TO	POTO	5Y: .	line	ar								
1107				n	mur.											
1108		(ii)	MOLE	COTE	TABI	s: p	rote:	ın								
1109																
1110		(xi)	SEQUI	ENCE	DES	CRIP	LION	: SE	O ID	NO:	26:					
1111			_		B	_	_	_	_	_	_		_			
1112	Asp Il	e Gln	Leu		Gln	Ser	Pro	Ser		Leu	Ser	Ala	Ser		Gly	
1113	1			5					10					15		
1114																
1115	Asp Th	r Val		Ile	Thr	Сув	Arg	Ala	Ser	Gln	Asp	Ile		Asn	Asn	
1116			20					25					30			
1117																
1118	Leu Va	_	_	Gln	Gln	Lys		Gly	Lys	Ala	Pro	_	Leu	Leu	I1e	
1119		35					40					45				
1120																
1121	Tyr Al	a Ala	Ser	Arg	Leu		Asp	G1y	Va1	Pro	Ser	Arg	Phe	Ser	G1y	
1122	5	0				55					60					
1123																
1124	Ser G1	y Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Pro	Val	Glu	Ala	
1125	65				70					75					80	
1126																
1127	Asp As	o Ala	Ala	Asp	Tyr	Tyr	Сув	Leu	G1n	Thr	Lys	Ser	Ser		Arg	
1128				85					90					95		
1129																
1130	Thr Ph	e Gly	G1n	Gly	Thr	Lys	Val	G1u	I1e	Lys	Arg					
1131			100					105								
1132																
1133	(2) I	NFORM	ATI01	N FOI	R SE	QI Q	NO:	27:								
1134																
1135	(	i) SE	QUEN	CE CI	IARA	CTER:	ISTI	CS:								
1136		(.	A) Li	ENGT	H: 32	24 b	ase p	paire	э							
1137		(	B) T	YPE:	nuc:	leic	acio	£								
1138		(	C) S	<b>TRAN</b> I	DEDNI	ESS:	botl	h								
1139		(	D) T(	OPOL	GY:	line	ear									
1140																
1141	(i	i) MO	LECU	LE T	YPE:	DNA	(gei	nomi	c)							
1142																
1143																
1144	(i	x) FE	ATURI	<b>E</b> :												

#### Raw Sequence Listing

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1145			NA!														
1146		(B)	) LO	CATIO	ON: 3	13	24										
1147																	
1148	(ix)	FEA:	TURE:	:													
1149		(A)	NA!	Æ/KI	EY: r	nat p	ept:	ide									
1150			LO														
1151																	
1152																	
1153	(xi)	SEO	TENCE	e DES	CRT	PTTO	J: SI	EO TI	O NO	: 27 :							
1154	(/							- ж,									
1155	GACATTCA	20 TO	ZACCO	' <b>ል</b> ርጥር	י דרי	תאאמי	MMM	NNN	MMM	ו אואו	NNN	NNN	וא או	MMM	MMM	a a	60
1156	01101111011	JC	J				1111111	111111		.,,,,,	11111111	.414141	.111 112	.12121212	.4111414	•	,
1157	NNNNNNNN	יוא אינ	STATATATA	TATATATA	תאתא צי	תתתתת	INININI	NININI	תתתת	ATATA I	TATATATI	TATA TATA	TN MI	ATATAKTAT	JAJAJAJA	<b>.</b>	120
1158	141414141414141	414 141	41414141	47474747	.1 11111	1111111	4111114	1414141	41414141	47474 1	414141	4111111	414 141	.41414141	.11111111	•	120
1159	NNNNNNN	TRT ND	TC3 C1	· · · · ·		nmm * r	10×0	C III III			7000	700	70 70	7000	73.77	-	180
1160	MMMMMMM	MIA 141	NCAG	-C-L	L GA.	LIIA	LGAG	GII.	LCCM	HCC (	3000	-16-16	3G A	31661	JAUA.	-	100
	* CCEE C * C	<b>.</b>	~ » ~ m ~	100m				mmai		mas :		** ~~	.~				240
1161	AGGTTCAG:	ru u	CAGT	3GGT(	J GG2	ACAC.	rgat	TTC	ACAC.	ICA I	AAAT	iA GC	AG A	31 GG/	AGGC1	ŗ	240
1162	~>~~	=~ ~ <i>.</i>	~~===					m. m.				. mma:			2000		200
1163 1164	GAGGATGT.	ru u	3611.	LATTA	I CI	SCAT	SCAA	TATA	ACAC	ACA .	LTCC	ATTC	AC I	TTCG	36666	-	300
	0003.0033			mera													324
1165	GGGACCAA	AC II	3(3M I I	TUM	A AC	3A.											344
1166 1167	(0) THE	\D1/1	T ( ) T	EOD	a E o	TD 1	70.01	٥.									
1168	(2) INF	JKMA.	LION	FUR	250	ID I	NU: 20	) ;									
	(4)	a mor	~=>-	- ATT		8 12 D T (		٦.									
1169	(1)	_	JENC						_								
1170			) LEI					acla	3								
1171			TY														
1172		(D)	TOI	ЮТОС	3¥: .	line	ar										
1173																	
1174	(ii)	MOL	ECOLI	TYI	BE: I	prote	ein										
1175																	
1176																	
1177																	
1178	(xi)	SEQI	UENC	E DES	SCRI	PTIO	V: 21	EQ II	ои с	:28:							
1179																	
1180	Aep	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Xaa		Xaa	Xaa	Xaa	Xaa		Xaa	
1181	1				5					10					15		
1182																	
1183	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
1184				20					25					30			
1185																	
1186	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	G1n	Pro	Leu	Ile	
1187			35					40					45				
1188																	
1189	Tyr	Glu	Va1	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro	Aep	Arg	Phe	Ser	Gly	
1190	•	50				J	55		•			60				_	
1191																	
1192	Ser	Glv	Ser	Aep	Thr	Asp	Phe	Thr	Leu	Lye	Ile	Ser	Arq	Va1	Glu	Ala	
1193	65	3				70				•	75					80	
1194						-					-						
1195	G1u	Asp	Va1	Glv	Va1	Tvr	Tyr	Cye	Met	G1n	Tyr	Thr	Hie	Ile	Pro	Phe	
1196					85		• -			90	•			_	95		

#### Raw Sequence Listing

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1197 1198 1199 1200 1201 1202	Th	r Pho	e Gl	y Pro 100	_	y Thi	г Гу	e Lei	u As <sub>]</sub>	-	e Lys	s Ar	3		
1203 1204 1205	(2) IN	FORM	ATIO	N FOI	R SE	Q ID	NO:	29:							
1206 1207 1208 1209 1210	(i	(1	_	engti Ype: Irani	H: 3: nucl	24 ba leic ESS:	aee j acio botl	paire d	e						
1211 1211 1212	(ii	, IOM (.													
1213 1214	-/	) НХІ					-								
1215 1216 1217 1218	(iv	·) AN	ri-sı	ense:	: NO										
1218 1219 1220	(ix	) FE2	ATURI A) N		KEY:	CDS									
1221 1222		(1	B) L	CAT	CON:	1	324								
1223 1224 1225	(xi	) SE(	QUEN	CE DI	ESCR:	[PTIC	ON: S	SEQ I	ID NO	0:29	:				
1226 1227 1228 1229	GAC ATT Asp Ile														48
1230 1231 1232	GAC AGA Aep Arg														96
1233 1234 1235 1236 1237	TTA AAT Leu Asn		Tyr					G1y							144
1238 1239 1240 1241	TAT GAG Tyr Glu 50	Val													192
1242 1243 1244 1245	AGT GGG Ser Gly 65														240
1246 1247 1248	GAG GAT Glu Asp														288

# Raw Sequence Listing

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1249   1250   ACT TTC GGC CCC GGG ACC ANA CTG GAT ATC ANA CGA   324   1251   Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg   105   105   105   1252   100   105   105   1254   1255   1254   (2) INFORMATION FOR SEQ ID NO:30:   1256   (a) LENGTH: 108 amino acids   (b) TYPE: amino acid   (b) TYPE: amino acid   (c) TYPE: amino acid   (d)
1251   Thr Phe Gly Pro Gly Thr Lys Leu App Ile Lys Arg   1252   100   105   105   105   1254   1254   1255   (2) INFORMATION FOR SEQ ID NO:30:   1256   (2) INFORMATION FOR SEQ ID NO:30:   1257   (3) SEQUENCE CHARACTERISTICS:   (3) LENGTH: 108 amino acids   (1259   (B) TYPE: amino acid   (D) TOPOLOGY: linear   1261   (11) MOLECULE TYPE: protein   1262   (11) MOLECULE TYPE: protein   1263   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:   15   10   15   15   10   15   15   10   15   15
1252 1254 1255 1256 1257 (2) INFORMATION FOR SEQ ID NO;30: 1256 1257 (3) LENGTH: 108 amino acids 1259 (B) TYPE: amino acid 1260 (D) TOPOLOGY: linear 1261 1262 (ii) MOLECULE TYPE: protein 1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO;30: 1265 1266 1267 1
1253 1254 1255 1256 1257 (i) SEQUENCE CHARACTERISTICS: 1258 (A) LENGTH: 108 amino acids 1259 (B) TYPE: amino acid 1260 (D) TOPOLOGY: linear 1261 1262 (ii) MOLECULE TYPE: protein 1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 135 40 45 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 1286 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pairs (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1254
1255 1256 1257 1258 (i) SEQUENCE CHARACTERISTICS: 1259 (ii) SEQUENCE CHARACTERISTICS: 1259 (iii) TOPOLOGY: linear 1261 1260 (ii) MOLECULE TYPE: protein 1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 1286 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: (a) LENGTH: 324 base pairs 1291 (b) TOPOLOGY: linear
1256 1257 (i) SEQUENCE CHARACTERISTICS: 1258 (a) LENGTH: 108 amino acids 1259 (B) TYPE: amino acid 1260 (D) TOPOLOGY: linear 1261 1262 (ii) MOLECULE TYPE: protein 1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45 1274 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95 1285 1286 (2) INFORMATION FOR SEQ ID NO:31 1288 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
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1260 (D) TOPOLOGY: linear 1261 1262 (ii) MOLECULE TYPE: protein 1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1261 1262 (ii) MOLECULE TYPE: protein 1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: Ilnear
1262
1263 1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 1265 1266
1265 1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1267 1 5 10 15 1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1266   Asp   Ile Gln   Leu Thr Gln   Ser Pro   Ser Ser   Leu   Ser   Ala   Ser   Val   Gly     1267   1
1267 1 5 10 15  1268  1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30  1271  1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45  1274  1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60  1277  1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80  1280  1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105  1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1268 1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30 1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45 1274 1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60 1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80 1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr 1270 20 25 30  1271  1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45  1274  1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60  1277  1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80  1280  1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105  1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  129  (a) LENGTH: 324 base pairs 1291 (b) TYPE: nucleic acid 1292 (c) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1270 1271 1272 1272 1272 1273 1274 1275 1274 1275 1277 1276 120 1277 1277 1278 1277 1278 1291 1291 1291 1291 1291 1291 1291 129
1271 1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273
1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile 1273 35 40 45  1274  1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276 50 55 60  1277  1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80  1280  1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1273
1274 1275    Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276    50    55    60 1277 1278    Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279    65    70    75    80 1280 1281    Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282    85    90    95 1283 1284    Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285    100    105 1286 1287    (2) INFORMATION FOR SEQ ID NO:31 1288 1289    (i) SEQUENCE CHARACTERISTICS: 1290    (A) LENGTH: 324 base pairs 1291    (B) Type: nucleic acid 1292    (C) STRANDEDNESS: both 1293    (D) TOPOLOGY: linear
1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly 1276
1276
1277 1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80  1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95  1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105  1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala 1279 65 70 75 80  1280  1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105  1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) Type: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1279 65 70 75 80  1280  1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105  1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) Type: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1280 1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe 1282 85 90 95 1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) Type: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe  1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg  1285 100 105  1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  1289 (i) SEQUENCE CHARACTERISTICS:  1290 (A) LENGTH: 324 base pairs  1291 (B) Type: nucleic acid  1292 (C) STRANDEDNESS: both  1293 (D) TOPOLOGY: linear
1282 85 90 95  1283  1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105  1286  1287 (2) INFORMATION FOR SEQ ID NO:31  1288  1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1283 1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg 1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1285 100 105 1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1286 1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1287 (2) INFORMATION FOR SEQ ID NO:31 1288 1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1288  1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1289 (i) SEQUENCE CHARACTERISTICS: 1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1290 (A) LENGTH: 324 base pairs 1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1291 (B) TYPE: nucleic acid 1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1292 (C) STRANDEDNESS: both 1293 (D) TOPOLOGY: linear
1293 (D) TOPOLOGY: linear
1294
1295 (ii) MOLECULE TYPE: cDNA
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1297 (iii) HYPOTHETICAL: NO
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#### Raw Sequence Listing

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1308 1309	a.a		~~~	ama		~~~	mam	~~	maa	maa	ama	mam	~~	mam	ama.	<i>a</i> a.	
				CTG													48
1310	_	TTE	GIN	Leu		GIN	ser	Pro	ser		тėл	ser	ATA	Ser		GIA	
1311	1				5					10					15		
1312	a.a	3.03	ama	300	3 000	3 am	mam	000	-	3 CM	<b>a</b> a	-	3 00 00		337		06
1313				ACC													96
1314	Asp	Thr	vai	Thr	TTE	Inr	cye	Arg		ser	GIN	GIY	TT6	_	Aen	Aen	
1315				20					25					30			
1316						a. a					a am				ama		144
1317				TAT													144
1318	Leu	Ala	_	Tyr	GIn	GIn	гля		GIY	гля	Ala	Pro	_	Arg	Leu	TTE	
1319			35					40					45				
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1321				TCC													192
1322	Tyr		Ala	Ser	Ser	Leu		ser	GIY	Val	Pro		Arg	Pne	ser	GIY	
1323		50					55					60					
1324	3 OM		mam	-	3.03	~ .	mma	3 am	ama	3.00	3 00 0		300	ama	~~	aam	240
1325				GGG													240
1326		GIA	ser	Gly	Thr		Pne	Thr	теп	Thr		ser	Ser	тéп	GIII		
1327	65					70					75					80	
1328	<i>-</i>	~			. am	m m	m. a	m < m	~~ *	~~~	~ m		3 Cm		aam	mma	200
1329				GCA													288
1330	GIU	Aep	Pne	A1a		lyr	Tyr	Сув	GIN		Авр	Aen	ser	TYT		Pne	
1331					85					90					95		
1332	3 am	mma	-	aa.	~~~	3.00	***	ama	a» a	a ma	* * *	00x					224
1333				GGA													324
1334 1335	Thr	Pne	GIY	Gly	GIA	Inr	гЛе	vaı		TTE	гля	Arg					
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1353			20					25					30			
1354 1355	Leu Ala	T	The ware	C15	~1 <sub>~</sub>	T	Dwo	C1	Y	310	D	T	3 mar	Y	T1.	
1356	Dec Ala	35		GIII	GTII	пув	40	GIY	пур	ATG	PLO	45	Arg	пец	116	
1357		23					10					43				
1358	Tyr Ale	310	Cor	Car	T.Ou	C1.	202	C1	37-1	Dro	Cor	3	Dha	C 0~	C1	
1359	50		261	Ser	пеп	55	Ser	Gry	Val	FIO	60	Arg	Fire	ser	GIY	
1360	50					,,,					50					
1361	Ser Gly	Ser	G1v	Thr	G111	Pho	Thr	T.011	Thr	T1_	Ser	Ser	T.011	G1n	Pro	
1362	65	DC2	07		70	1110	1111	шец	-11L	75	501	501	200	Gan	80	
1363	03				, 0					, 3						
1364	Glu Asp	Phe	A1a	Thr	Tvr	Tvr	Cvs	G1n	G1n	Ago	Asn	Ser	Tvr	Pro	Phe	
1365	<b>-</b>			85	-2-	-4-	-2-		90				-1-	95		
1366																
1367	Thr Phe	G1v	G1v	G1v	Thr	Lvs	Val	G1u	I1e	Lvs	Ara					
1368			100	1		-1-		105		-,-						
1369																
1370	(2) IN	FORM	ATIO	N FOI	R SEC	O ID	NO:	33								
1371		_				-		-								
1372	(i	) SE	OUEN	CE CI	IARA(	CTER	ISTI	CS:								
1373				ENGTI					5							
1374				YPE:			-									
1375			-	TRANI												
1376		(1	D) T	OPOL	GY:	line	ear									
1377																
1378	(ii	) MO	LECU	LE T	YPE:	cDN	A									
1379																
1380	(iii	) HY	POTH	ETIC	AL: 1	10										
1381																
1382	(iv	) AN	ri-si	ENSE:	: NO											
1383																
1384																
1385	(ix	) FE														
1386				AME/I												
1387		()	B) L	CAT:	CON:	1	324									
1388																
1389																
1390	(xi	) SE	QUEN(	CE DE	SCR	[PTI	ЭМ:	SEQ 3	ID NO	0:33						
1391																
1392	GAC ATT															48
1393	Asp Ile	Gln	Leu		Gln	Ser	Pro	Ser		Leu	Ser	Ala	Ser		Gly	
1394	1			5					10					15		
1395																
1396	GAC ACA															96
1397	Asp Thr	Val		Ile	Thr	Сув	Arg		Ser	Gln	Gly	Ile		Asn	Asn	
1398			20					25					30			
1399	mm :	TT	m =	<i>~~</i>	a= ~		~~-	~~=		~~~	~~~	~		am~		444
1400	TTA GCC															144
1401	Leu Ala	_	TYT	GIN	GIN	гЛа		GTĀ	гЛа	ATA	PTO		arg	ьeц	тте	
1402 1403		35					40					45				
	TAT GCT	CCA	m///	N CHIT	mma	CAN	N CITT	aaa	CITIC!	aas	ጥረተጽ	100	ጥጥረግ	N CVIT	cec	192
1404	INI GCI	G CAS	100	AGI	116	GMM	AG#	333	GAC	- was	LCA	DUA	110	LUA	330	172

#### Raw Sequence Listing

06/27/93 13:09:22 s5963.raw

1405	Tyr	A1a	A1a	Ser	Ser	Leu	G1u	Ser	G1y	Va1	Pro	Ser	Arg	Phe	Ser	Gly	
1406		50					55					60					
1407																	
1408					ACA												240
1409		G1y	Ser	Gly	Thr		Phe	Thr	Leu	Thr		Ser	Ser	Leu	Gln		
1410	65					70					75					80	
1411																	
1412					ACT												288
1413	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln		qaA	Asn	Ser	Tyr		Phe	
1414					85					90					95		
1415																	
1416					GGG												324
1417	Thr	Phe	Gly	_	G1y	Thr	Lys	Val	Glu	Ile	Lys	Arg					
1418				100					105								
1419																	
1420																	
1421	(2)	IN	FORM	ATIO1	I FOI	R SE	) ID	NO:	34								
1422																	
1423			(i) S		ENCE												
1424					LEI					acida	3						
1425					TYI												
1426				(D)	TOI	OTO	Y: .	line	ar								
1427																	
1428		(:	ii) 1	OLE	CULE	TYPI	: pı	rote:	in								
1429																	
1430		(2	ki) S	EQUI	ENCE	DESC	CRIP	CION	: SE(	Q ID	NO:	34					
1431																	
1432	Asp	I1e	G1n	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1433	1			•	5					10					15		
1434																	
1435	Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg		Ser	Gln	Gly	Ile		Asn	Asn	
1436				20					25					30			
1437																	
1438	Leu	A1a	Trp	Tyr	Gln	G1n	Lys	Pro	G1y	Lys	Ala	Pro	Lys	Arg	Leu	Ile	
1439			35					40					45				
1440																	
1441	Tyr	A1a	A1a	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
1442		50					55					60					
1443																	
1444	Ser	G1y	Ser	G1y	Thr	Glu	Phe	Thr	Leu	Thr	I1e	Ser	Ser	Leu	Gln	Pro	
1445	65					70					75					80	
1446																	
1447	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Сув	Gln	Gln	Asp	Asn	Ser	Tyr	Pro	Phe	
1448		_			85					90					95		
1449																	
1450	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Va1	Glu	Ile	Lys	Arg					
1451			_	100	_		-		105		•	_					
1452																	
1453	(2)	IN	FORM	ATIO	N FO	R SE	Q ID	NO:	35:								
1454																	
1455		(i)	) SE(	QUEN	CE CI	IARA(	CTER:	ISTI	CS:								
1456			(2	A) LI	ENGT	H: 34	12 ba	ase j	pair	S							
								-									

#### Raw Sequence Listing

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1457 1458				3) T: 2) S:													
1459			(1	) T	DPOL	OGY:	lin	sar									
1460		122					- 537										
1461 1462		(11	) MO.	LECU	LE T	TPE:	CDN	A.									
1463																	
1464		(ix	FE	ATURI	Ξ:												
1465				A) N2		KEY:	CDS										
1466				B) L(				342									
1467																	
1468																	
1469		(xi	) SE	QUEN	CE DI	ESCR:	IPTI	on:	SEQ :	ID N	0:35	:					
1470																	
1471											_	_	_		GCA	_	48
1472		Ils	Val	Mst		Gln	Ssr	Pro	Thr		Lsu	Ala	Val	Thr	Ala	Ssr	
1473 1474	1				5					10					15		
1475	220	330	ame.	N.C.C	א חיידי א	A CITT	TCC	አረጥ	acc	TO T	CAC	N.C.C	Cumm	ייי מייי	TCA	N.C.C	96
1476															Ser		30
1477	-7	-,-		20			<b>-1</b>	- 11-	25	502	<b>01</b> 4			30		001	
1478														•			
1479	AAA	CAC	AAG	GTG	CAC	TAC	TTG	GCT	TGG	TAC	CAG	AAG	AAA	CCA	GAG	CAA	144
1480	Lys	His	Lys	Va1	His	Tyr	Leu	Ala	Trp	Tyr	G1n	Lys	Lys	Pro	G1u	G1n	
1481			35					40					45				
1482																	
1483															GGG		192
1484	Ser		Lys	Leu	Leu	Ile	_	Gly	Ala	Ssr	Asn		Tyr	Ile	Gly	Va1	
1485		50					55					60					
1486						~~~	- ~-	~~:	_ ~_	~~~		~~ =			~~~		0.40
1487															CTG		240
1488 1489	65	Авр	Arg	Pns	THE	70	SHI	GLY	SBL	GIA	75	ABD	Pne	THE	Lsu	80	
1490	0.5					, 0					, 5					00	
1491	ATC	AGC	AGT	GTA	CAG	GTT	GAA	GAC	CTC	ACA	CAT	TAT	TAC	TGT	GCA	CAG	288
1492															Ala		
1493					85			_		90		•	•		95		
1494																	
1495															GAG		336
1496	Phs	Tyr	Ser	Tyr	Pro	Leu	Thr	Phe		Ala	G1y	Thr	Lys		Glu	Lsu	
1497				100					105					110			
1498																	2.40
1499		CGG															342
1500	га	Arg															
1501 1502																	
1502																	
1504	(2)	) IN	FORM	ATIO	T FOI	R SEC	ם ב	NO:	36:								
1505	, 2	,	· Orden		. 201				•								
1506			(i) :	SEQUI	ENCE	CHAI	RACT	ERIS:	rics	:							
1507									ino a		8						
1508				(B)	TY	PE: a	amino	ac:	id								

#### Raw Sequence Listing

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1509				(D)	TOI	POLO	GY: :	linea	ar							
1510 1511			ii) 1	KOT.E	ים.דוני	ומעייי	. n		<b>.</b> ~							
1512		,,	**, :	MOLLE	20115	* 7 5 1	a. p.	LOCE.	***							
1513		(:	xi) s	SEQUI	ENCE	DESC	CRIP:	rion:	SE(	2 ID	NO:	36:				
1514										-						
1515	Asp	Ile	Va1	Met	Thr	G1n	Ser	Pro	Thr	Phe	Leu	A1a	Va1	Thr	A1a	Ser
1516	1				5					10					15	
1517		_											_	_		
1518	Lys	Lys	Val		Ile	Ser	Сув	Thr		Ser	Glu	Ser	Leu	_	Ser	Ser
1519 1520				20					25					30		
1521	Tara	uie	Lys	17-1	ui a	Tree	T.611	21 a	Trn	Tree	Gln	Larg	Larg	Bro	Glu.	Gln
1522	пув	11120	35	Val	1115	TYT	пец	40	пр	TYL	GIII	пур	45	FIG	GIU	GIII
1523			•													
1524	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Ile	G1y	Val
1525		50	•				55	•				60	•		_	
1526																
1527	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
1528	65					70					75					80
1529									_		•					
1530	Ile	Ser	Ser	Val		Val	Glu	Asp	Leu		His	Tyr	Tyr	Cys		Gln
1531 1532					85					90					95	
1532 1533	Bho	There	Ser	The same	Dec	Lon	The	Bho	C112	<b>81</b> -	C112	Th.	Tara	Lon	C1.	Lou
1534	Pne	TAL	Ser	100	PIQ	пеп	III	Pne	105	AId	GIY	IIII	пув	110	GIU	nen
1535				-00					103							
1536	Lvs	Arg		v												
1537	•			•												
1538																
1539	(2	INI	FORM	OITA	I FOI	R SE	] ID	NO:	37:							
1540																
1541		(i)		QUEN												
1542				A) LI				_		3						
1543				B) T:	YPE: FRANI											
1544 1545			-	C) SI O) T(					1							
1546			(1	<i>)</i> , 10	)FQII(	JGI:	T T 77.5	a.								
1547		(ii	) MOI	LECUI	E TY	YPE:	cDN	4								
1548		`	,				<b>U</b>	-								
1549		(iii)	HYI	POTH	STIC	AL: 1	NO									
1550																
1551		(iv)	AN'	ri-Si	ENSE	: NO										
1552																
1553			_													
1554		(ix	) FEA				ar c									
1555			-	A) NZ	-			200								
1556 1557			(1	B) L(	JCAT'	FON:	1	24/								
1557 1558																
1559		(xi	) SE(	DEN	E DI	SSCR'	[PTTC	on: 9	SEO 1	ED NO	0:37					
1560		,	,1				·	•	<b>z</b>							

#### Raw Sequence Listing

06/27/93 13:09:43 S5963.raw

1561 1562 1563 1564			GTG Val													GGA Gly	48
1565 1566 1567 1568			GTC Val														96
1569 1570 1571 1572			TGG Trp 35														144
1573 1574 1575 1576			GCA Ala														192
1577 1578 1579 1580			TCT Ser														240
1581 1582 1583 1584			GCT Ala														288
1585 1586 1587 1588			TTC Phe														327
1589 1590 1591	(2)	INI	FORM	ATION	I FOF	R SEÇ	) ID	NO:3	88:								
1592 1593 1594 1595			(i) S	(A) (B)	ENCE LEN TYI TOI	IGTH:	109 mino	ami	ino a		3						
1596 1597 1598			Li) N				Ī										
1599 1600 1601	Ala		ci) S Val										Ala	Ala	Val	G1y	
1602 1603 1604	1				5					10					15		
1605 1606	GIY	Inc	Val	20	TTG	гур	сув	GIN	25	ser	GIU	АВП	116	30	ser	Set	
1607 1608 1609	Leu	Ala	Trp 35	Tyr	G1n	Gln	Lys	Pro 40	Gly	G1n	Pro	Pro	Lys 45	Leu	Leu	Ile	
1610 1611 1612	Tyr	G1y 50	A1a	Ser	Thr	Leu	<b>A1</b> a 55	Ser	G1y	Va1	Pro	Ser 60	Arg	Phe	Lys	G1y	

# Raw Sequence Listing

06/27/93 13:09:49 S5963.raw

1614 1615	Ser Arg	, Ser	Gly	Thr	Glu 70	Tyr	Thr	Leu	Thr	11e 75	Ser	Gly	Va1	G1n	Arg 80	
1616 1617	Glu As	Ala	Ala	Thr 85	Tyr	Tyr	Сув	Leu	Gly 90	Ser	qaA	Ser	Ser	Ser 95	Asp	
1618 1619 1620	Thr Ala	Phe	Gly 100	Gly	Gly	Thr	Glu	Leu 105	Glu	Ile	Leu	Сув				
1621 1622 1623	(2) ĮI	IFORM	ATIO	N FOI	R SE	Q IĐ	NO:	39:								
1624 1625	(:	) SE	QUEN( A) Li							>>	رح°	0		15	Sted	
1626		-	B) T				-				_			, ,		-
1627			c) s:													
1628		(	D) T	OPOL	OGY:	line	ar									
1629																
1630	(i:	L) MO	LECU:	LE T	YPE:	cDN2	A.									
1631		_														
1632	(11:	.) HY	POTH	ETIC	AL: 1	10										
1633	(4-	_\	mT 4		370											
1634	(17	r) AN	11-5	ENSE	: NO											
1635 1636																
1637	14.	c) FE.	ימדוייה	<b>.</b>												
1638	1,22		A) N		ZEV.	CDG										
1639			B) Le	-			321									
			_, _													
1640																
1640 1641																
1641	(x:	.) SE						SEO :	ID NO	0:39						
	(x:	.) SE						SEQ :	ID NO	D:39	:					
1641 1642	(x:		QUEN	CE DI	ESCR:	[PTI	ON: 4					TCT	GAT	GAG	CAG	48
1641 1642 1643		GCT	QUEN GCA	CE DI	escr: Tct	IPTI(	ON: 8	ATC	TTC	CCG	CCA					48
1641 1642 1643 1644	ACT GT	GCT	QUEN GCA	CE DI	escr: Tct	IPTI(	ON: 8	ATC	TTC	CCG	CCA					48
1641 1642 1643 1644 1645	ACT GTO	GCT	QUEN GCA	CE DI CCA Pro	escr: Tct	IPTI(	ON: 8	ATC	TTC Phe	CCG	CCA			Glu		48
1641 1642 1643 1644 1645 1646	ACT GTO Thr Val	GCT Ala	QUEN GCA Ala GGA	CE DI CCA Pro 5	ESCR: TCT Ser GCC	GTC Val	ON: 6 TTC Phe	ATC Ile	TTC Phe 10 TGC	CCG Pro	CCA Pro	Ser	Asp	Glu 15 TTC	Gln TAT	48
1641 1642 1643 1644 1645 1646 1647 1648 1649	ACT GTO Thr Val	GCT Ala	QUENG GCA Ala GGA Gly	CE DI CCA Pro 5	ESCR: TCT Ser GCC	GTC Val	ON: 6 TTC Phe	ATC Ile	TTC Phe 10 TGC	CCG Pro	CCA Pro	Ser	Asp AAC Asn	Glu 15 TTC	Gln TAT	
1641 1642 1643 1644 1645 1646 1647 1648 1649 1650	ACT GTO Thr Val	GCT Ala	QUEN GCA Ala GGA	CE DI CCA Pro 5	ESCR: TCT Ser GCC	GTC Val	ON: 6 TTC Phe	ATC Ile	TTC Phe 10 TGC	CCG Pro	CCA Pro	Ser	Asp	Glu 15 TTC	Gln TAT	
1641 1642 1643 1644 1645 1646 1647 1648 1649 1650	ACT GTO Thr Val 1 TTG AAI Leu Lys	GCT Ala TCT Ser	QUENC GCA Ala GGA Gly 20	CCA Pro 5 ACT	ESCR: TCT Ser GCC Ala	GTC Val TCT Ser	TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn	Asp AAC Asn 30	Glu 15 TTC Phe	Gln TAT Tyr	96
1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651	ACT GTO Thr Val  TTG AAA Leu Lys	GCT Ala TCT Ser	GCA Ala GGA Gly 20 GCC	CE DI CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	ON: 6 TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn GCC	AAC ABN 30	Glu 15 TTC Phe	Gln TAT Tyr TCG	
1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652	ACT GTO Thr Val 1 TTG AAI Leu Lys	GCT Ala TCT Ser	GCA Ala GGA Gly 20 GCC	CE DI CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	TTC Phe GTT Val TGG Trp	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	AAT Asn GCC Ala	AAC ABN 30	Glu 15 TTC Phe	Gln TAT Tyr TCG	96
1641 1642 1643 1644 1645 1646 1647 1648 1659 1651 1652 1653 1654	ACT GTO Thr Val  TTG AAA Leu Lys	GCT Ala TCT Ser	GCA Ala GGA Gly 20 GCC	CE DI CCA Pro 5 ACT Thr	TCT Ser GCC Ala	GTC Val TCT Ser	ON: 6 TTC Phe GTT Val	ATC Ile GTG Val 25	TTC Phe 10 TGC Cys	CCG Pro CTG Leu	CCA Pro CTG Leu	Ser AAT Asn GCC	AAC ABN 30	Glu 15 TTC Phe	Gln TAT Tyr TCG	96
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655	ACT GTO Thr Val  TTG AAI Leu Lys  CCC AGS	GCT Ala TCT Ser GAG Glu 35	QUENG GCA Ala GGA Gly 20 GCC Ala	CE DI CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln	ON: STTC Phe GTT Val TGG Trp 40	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT Asn GCC Ala 45	AAC ABN 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96 144
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655	ACT GTO Thr Val  TTG AAI Leu Lys  CCC AGS Pro Arg	GCT Ala TCT Ser GAG GAG GIU 35	QUENG GCA Ala GGA Gly 20 GCC Ala	CE DI CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln	ON: STTC Phe GTT Val TGG Trp 40 ACA	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT ASN GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655 1656	ACT GTO Thr Val  TTG AAA Leu Lys  CCC AGA Pro Arg	GCT Ala TCT Ser GAG GAG GIU 35 TCC	QUENG GCA Ala GGA Gly 20 GCC Ala	CE DI CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln GTC Val	ON: STTC Phe GTT Val TGG Trp 40 ACA	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT ASN GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96 144
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1654 1655 1656 1657 1658	ACT GTO Thr Val  TTG AAI Leu Lys  CCC AGS Pro Arg	GCT Ala TCT Ser GAG GAG GIU 35 TCC	QUENG GCA Ala GGA Gly 20 GCC Ala	CE DI CCA Pro 5 ACT Thr AAA Lys	TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln	ON: STTC Phe GTT Val TGG Trp 40 ACA	ATC Ile GTG Val 25 AAG Lys	TTC Phe 10 TGC Cys GTG Val	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn	AAT ASN GCC Ala 45	AAC Asn 30 CTC Leu	Glu 15 TTC Phe CAA Gln	Gln TAT Tyr TCG Ser	96 144
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1656 1657 1658	ACT GTO Thr Val  TTG AAA Leu Lys  CCC AGS Pro Arg	GCT Ala TCT Ser GAG Glu 35	QUENG GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DI CCA Pro 5 ACT Thr AAA Lys GAG Glu	ESCR: TCT Ser GCC Ala GTA Val	GTC Val TCT Ser CAG Gln GTC Val	ON: STTC Phe GTT Val TGG Trp 40 ACA	ATC Ile GTG Val 25 AAG LyB GAG Glu	TTC Phe 10 TGC Cys GTG Val CAG Gln	CCG Pro CTG Leu GAT ABP	CCA Pro CTG Leu AAC ABn	AAT Asn GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC Asp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144 192
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1656 1657 1658 1659 1660	ACT GTO Thr Val  TTG AAA Leu Lys  CCC AGS Pro Arg  GGT AAG Gly Ass 50  TAC AGG	GCT Ala TCT Ser GAG Glu 35 TCC Ser	QUENC GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DI CCA Pro 5 ACT Thr AAA Lys GAG Glu AGC	ESCR: TCT Ser GCC Ala GTA Val AGT Ser	GTC Val TCT Ser CAG Gln GTC Val 55	ON: STTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn AGC Ser 60	AAT ABN GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC ASp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1656 1657 1658 1659 1660 1661	ACT GTO Thr Val  TTG AAA Leu Lys  CCC AGS Pro Arg  GGT AAG Gly Ass  TAC AGG Tyr Ses	GCT Ala TCT Ser GAG Glu 35 TCC Ser	QUENC GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DI CCA Pro 5 ACT Thr AAA Lys GAG Glu AGC	ESCR: TCT Ser GCC Ala GTA Val AGT Ser ACC Thr	GTC Val TCT Ser CAG Gln GTC Val 55	ON: STTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC	CCG Pro CTG Leu GAT Asp GAC Asp	CCA Pro CTG Leu AAC ABn AGC Ser 60	AAT ABN GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC ASp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144 192
1641 1642 1643 1644 1645 1646 1647 1648 1650 1651 1652 1653 1655 1655 1656 1657 1658 1659 1660	ACT GTO Thr Val  TTG AAA Leu Lys  CCC AGS Pro Arg  GGT AAG Gly Ass 50  TAC AGG	GCT Ala TCT Ser GAG Glu 35 TCC Ser	QUENC GCA Ala GGA Gly 20 GCC Ala CAG Gln	CE DI CCA Pro 5 ACT Thr AAA Lys GAG Glu AGC	ESCR: TCT Ser GCC Ala GTA Val AGT Ser	GTC Val TCT Ser CAG Gln GTC Val 55	ON: STTC Phe GTT Val TGG Trp 40 ACA Thr	ATC Ile GTG Val 25 AAG Lys GAG Glu	TTC Phe 10 TGC Cys GTG Val CAG Gln AGC	CCG Pro CTG Leu GAT Asp	CCA Pro CTG Leu AAC ABn AGC Ser 60	AAT ABN GCC Ala 45 AAG Lys	AAC Asn 30 CTC Leu GAC ASp	Glu 15 TTC Phe CAA Gln AGC Ser	Gln TAT Tyr TCG Ser ACC Thr	96 144 192

Raw Sequence Listing

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1665	Hie	Lye	Va1	Tyr		Суе	G1u	Va1	Thr		G1n	Gly	Leu	Ser		Pro	
1666					85					90					95		
1667															/		(
1668				, AGC							TA				(-		( 321 )
1669	Val	Thr	Lye	Ser	Phe	Aen	Arg	Gly		Cys					_	~	
1670				100					105								200
1671										-							520
1672																	
1673	(2	) IN	FORM	ATIO	N FO	R SE	2 ID	NO:	40:								- WC 115-4
1674			,														
1675			(1)	SEQU							_						@ 12.62 (·
1676					) LE					acid	e						on this li
1677					) TY												•
1678				(D	) TO	SOTO	GI: .	line	ar								
1679		,	221	VOT T	II	murn:	<b>.</b>		•								
1680		(	11)	MOLE	COPE	TYP	s: p	rote	ın								
1681				death	EST 619	DEG.	45 T 51	TT 017	. 454	A =D							
1682		(.	X1)	SEQU	en Cr	DED	-KIP	LION	: DE	מד מ	NO:	10:					
1683 1684	mb	37-1	21-	31.	Dwa	Com	77-7	Dho	т1.	Dho	Dma	Dma	Com	2 00	<b>C1</b>	C1-	
1685	1	Val	ATG	Ala		ser	Val	File	TIE	10	PIO	PLO	ser	web	15	GIII	
1686	_				5					10					10		
1687	T.An	Taro	C 0.7	Gly	mb-s	212	Can	77~7	17-3	Cara	Tarr	Lan	7	7 00	Dho	T	
1688	ne u	пус	Del	20	1111	AIG	DOT	Val	25	Cya	пеп	пeп	VĆII	30	LIIG	<u> </u>	
1689				20					23					30			
1690	Pro	Ara	Glu	Ala	T.VA	Val	Gln	Trn	Tve	Val	Aen	Aen	Δla	T.e.11	Gln	Ser	
1691		9	35		776	***	0211	40	<b>-</b> y -	, C. T.	nep.	nen	45	. 200	0111	D-C1	
1692								10					1.5				
1693	Glv	Aen	Ser	Gln	G111	Ser	Val	Thr	Glu	Gln	Aep	Ser	Lve	Aep	Ser	Thr	
1694	1	50					55					60	-7 -				
1695		•					-					•					
1696	Tvr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lve	Ala	Aep	Tvr	Glu	Lve	
1697	65					70					75					80	
1698																	
1699	Hie	Lys	Val	Tyr	Ala	Cye	Glu	Val	Thr	Hie	Gln	Gly	Leu	Ser	Ser	Pro	•
1700		•		-	85	•				90		•			95		
1701																	
1702	Va1	Thr	Lye	Ser	Phe	Aen	Arg	Gly	Glu	Cye							
1703				100			_	_	105	_							
1704																	
1705																	
1706	(2	) IN	FORM	ATIO	N FO	R SE	Q ID	NO:	41:								
1707																	
1708		(i		QUEN								¬ ~		_		. ــــــــــــــــــــــــــــــــــــ	
1709				A) Li						e	)	2	2	ري		] [ [	Szed
1710				B) T								_		-		. , .	
1711			-	C) S'					h								
1712			(	D) T	OPOL	GY:	line	ear									
1713																	
1714		(ii	) MO	LECU	LE T	YPE:	cDN	A.									
1715																	
1716		(iii	) HY	POTH	ETIC	AL: Y	YES										

1767

#### Raw Sequence Listing

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#### Patent Application US/07/952,640

1717																	
1718		(iv)	AN'	ri~s	ense	: NO											
1719																	
1720																	
1721		(ix)	) FE	ATUR!	E:												
1722		•			AME/I	KEY:	CDS										
1723					OCAT:			321									
1724			•	-, <u>-</u>													
1725																	
1726		(wi)	SEC	OHEN	CE D	EGCD.	тртт	ON.	SRO '	א מד	0 • 41						
1727		(11)	, D.	20221	CB D.	ab CIV.			, <u>y</u>	LD 11	V. 11	•					
1728	CCT	GTG	COT	CCA	CCA	тст	CTC	TTC	ATC	ጥጥረ	cca	CCA	T/T	GAG	CAT	CAG	48
1729				_	Pro										-		40
1730	1	Val	ALG	ATA	5	Per	AGT	FIIG	TTE	10	PLO	PIO	ser	GIU	15	GIII	
1731	_				,					10					13		
1732	CEC	222	m/cm	CCN	2 (10)	ama.	m/cm		CTC C	maa.	ama.	CEC	3 % ED	330	mm/C	m a m	96
					ACT												36
1733	val	гЛа	ser	_	Thr	val	ser	val		Cys	тел	теп	ASII		Pne	Tyr	
1734				20					25					30			
1735																	2.44
1736					AGC								_				144
1737	Pro	Arg		Ala	Ser	Val	Lys	_	Lys	Val	Asp	Gly		Leu	Lys	Thr	
1738			35					40					45				
1739																	
1740					GAG												192
1741	Asp		Ser	Gln	Glu	Ser		Thr	Glu	Gln	Asp		Lys	Asp	Asn	Thr	
1742		50					55					60					
1743																	
1744	TAC	AGC	CTG	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AGC	ACA	GAC	TAC	CAG	AGT	240
1745	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Ser	Thr	Asp	Tyr	Gln	Ser	
1746	65					70					75					80	
1747																	
1748	CAC	AAT	GTC	TAT	GCC	TGC	GAA	GTC	ACC	CAT	CAG	GGC	CTG	AGC	TCG	CCC	288
1749	His	Asn	Val	Tyr	A1a	Cys	G1u	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	•
1750					85					90					95		
1751																	
1752	GTC	ACC	AAG	AGC	TTC	AAC	AGG	GGA	GAG	TGT	TA						$\begin{pmatrix} 321 \end{pmatrix} - \begin{pmatrix} 1 \end{pmatrix}$
1753	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Сув							$\begin{pmatrix} 321 \\ 2 \end{pmatrix} $
1754			_	100			_	_	105	_							5 2
1755																	
1756																	
1757	(2)	INI	FORM	ATIO	N FO	R SE	O ID	NO:	42:								
1758						,	_										
1759			(i)	SEOU	ENCE	CHAI	RACT:	ERIS'	rics	:							
1760					) LEI						s						•
1761					) TY						-						
1762					TO												
1763				,	,		•										
1764		1-	1111	MOT.F	CULE	TVD	E: n	rote	in								
1765		٠,-	, .		تدبب		<sub>P</sub> .										
1766		1-	r#1 (	g PAIT	ENCE	DRG	ים ד סי׳	יאר) דיי	. CP/	מד כ	NO	42.					
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1768 Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln

# Raw Sequence Listing

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1769	1				5					10					15		
1770																	
1771	Va1	Lys	Ser	G1y	Thr	Va1	Ser	Va1	Va1	Сув	Leu	Leu	Asn	Asn	Phe	Tyr	
1772				20					25					30			
1773																	
1774	Pro	Arg	G1u	A1a	Ser	Va1	Lys	Trp	Lys	Va1	Asp	G1y	Ala	Leu	Lys	Thr	
1775			35					40					45				
1776																	
1777	Asp	Asn	Ser	G1n	G1u	Ser	Va1	Thr	G1u	G1n	Asp	Ser	Lys	Asp	Asn	Thr	
1778	_	50					55				_	60	_	_			
1779																	
1780	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Ser	Thr	Asp	Tyr	G1n	Ser	
1781	65					70					75		_	_		80	
1782																	
1783	His	Asn	Va1	Tyr	A1a	Сув	G1u	Va1	Thr	His	G1n	G1y	Leu	Ser	Ser	Pro	
1784				•	85	•				90					95		
1785																	
1786	Va1	Thr	Lys	Ser	Phe	Asn	Arq	G1v	G1u	Cvs							
1787			•	100					105	-4-							
1788																	
1789																	
1790	(2)	IN	FORM	ATIO	N FOI	R SEC	O ID	NO:	43:								
1791	•						•	_									
1792		(i	) SE	OUEN	CE CI	IARA	TER:	ISTI	cs:	_	_		. ,	_			Λ
1793		•		_	ENGTI					3	>	54	$\mathcal{L}$	<b>'</b> )	1	<pre>(</pre> .	fed
1794					YPE:						•				,	1	<del></del>
1795					rani												
1796					POL												
1797			•	-, -													
1798		(ii	) MOI	LECUI	LE T	YPE:	cDN	A									
1799		•						-									
1800		(111	HY	POTH	ETIC	AL: 1	10										
1801																	
1802		(iv	AN'	ri-si	ENSE	: NO											
1803		,	,														
1804																	
1805		(ix	) FE	ATURI	R:												
1806		,	*		AME/I	CRY:	CDS										
1807					CAT:			321									
1808			``	-, -			_,,,										
1809																	
1810							гртта	3M.	ero :	ED NO	0:43						
		(xi	) SEC	OUEN	CE DI	35CR.		J11 -	360 .			•					
TRTT		(xi	) SE	QUEN	CE DI	sscr.		)14: ·	. gae			•					
1811 1812	GΆΤ	·		-					_				TCT	GCT	GAT	CAG	48
1812		CCA	ATT	GCG	CCT	ACT	GTC	CTC	CTC	TTC	CCA	CCA					48
1812 1813	Asp	CCA		GCG	CCT Pro	ACT	GTC	CTC	CTC	TTC Phe	CCA	CCA			Asp		4.8
1812 1813 1814		CCA	ATT	GCG	CCT	ACT	GTC	CTC	CTC	TTC	CCA	CCA					48
1812 1813 1814 1815	Asp 1	CCA Pro	ATT Ile	GCG Ala	CCT Pro 5	ACT Thr	GTC Val	CTC Leu	CTC	TTC Phe 10	CCA Pro	CCA Pro	Ser	Ala	Asp 15	G1n	
1812 1813 1814 1815 1816	Asp 1 CTG	CCA Pro	ATT Ile	GCG Ala GAA	CCT Pro 5	ACT Thr	GTC Val	CTC Leu ATC	CTC Leu GTG	TTC Phe 10 TGC	CCA Pro	CCA Pro	Ser AAT	Ala AAA	Asp 15 TTC	Gln CGT	<b>4</b> 8
1812 1813 1814 1815 1816 1817	Asp 1 CTG	CCA Pro	ATT Ile	GCG Ala GAA Glu	CCT Pro 5	ACT Thr	GTC Val	CTC Leu ATC	CTC Leu GTG Val	TTC Phe 10 TGC	CCA Pro	CCA Pro	Ser AAT	Ala AAA Lys	Asp 15 TTC	Gln CGT	
1812 1813 1814 1815 1816 1817 1818	Asp 1 CTG	CCA Pro	ATT Ile	GCG Ala GAA	CCT Pro 5	ACT Thr	GTC Val	CTC Leu ATC	CTC Leu GTG	TTC Phe 10 TGC	CCA Pro	CCA Pro	Ser AAT	Ala AAA	Asp 15 TTC	Gln CGT	
1812 1813 1814 1815 1816 1817	Asp 1 CTG Leu	CCA Pro ACA Thr	ATT Ile	GCG Ala GAA Glu 20	CCT Pro 5 ACA Thr	ACT Thr GTC Val	GTC Val ACC Thr	CTC Leu ATC Ile	CTC Leu GTG Va1 25	TTC Phe 10 TGC Cys	CCA Pro GTG Val	CCA Pro GCA Ala	Ser AAT Asn	AAA Lys 30	Asp 15 TTC Phe	Gln CGT Arg	

#### Raw Sequence Listing

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1821 1822	Pro	Asn	Asp 35	Ile	Thr	Val	Thr	Trp	Lys	Va1	Asp	Asp	Glu 45	Ile	Gln	Gln	
1823			33					40					43				
1824	ACC	ccc	TTC	GAG	220	) CT	ልሮኔ	ልሮኔ	CCG	CAG	A CC	ccc	GAG	GAC	ጥርሞ	ACC	192
1825			Phe														1.72
1826	Der	50	2116	G., u	ADII	DOL	55	T 111		94.11	DOT	60	GIG	vob	Cyb	T 11T	
1827		30										00					
1828	тъс	AAC	CTC	AGC	AGC.	ΣСТ	CTC	ጥሮኔ	СТС	ACC	222	CCA	CAG	тъс	AAC	ACC	240
1829			Leu														240
1830	65	non	пец	Der	561	70	пец	Der	пеп		75	ALG	9111	-7-	ADII	80	
1831						, ,					, ,					00	
1832	CAC	A GC	GTG	тас	ACC	TGC	GAG	GTG	GTC	ሮኔጥ	CAC	AAC	TCG	GGC	TCA	ccc	288
1833			Val														200
1834			142	-1-	85	O, C	014	7 44 2	142	90	*****	11044	502		95	214	
1835															-		
1836	ATC	GTC	CAG	AGC	TTC	AAT	AGG	GGT	GAC	TGT	TA						321
1837			Gln														( )
1838		142	· · · · ·	100			5	<b>0-</b> 1	105	٠,٠							
1839																	
1840																	
1841	(2)	TNI	ORM	וחדתב	J HOI	SEC	חד נ	NO	44 •								
1842	\_,		· Oldin				¿										
1843			(i)	SEOUI	ENCE	CHAI	RACTI	RIS	TICS:								
1844			\ <b>-</b> / -						ino a		8						
1845						PE: a					_						
1846						POLO											
1847				,-,													
1848		(:	ii) M	MOLE	TULE	TYPE	: p:	rote	in								
1849		•															
1850		(2	ci) S	EOUI	ENCE	DESC	RIP:	CION	: SEC	) ID	NO:	14:					
1851		·	•	-						•							
1852	Asp	Pro	Ile	Ala	Pro	Thr	Va1	Leu	Leu	Phe	Pro	Pro	Ser	Ala	Asp	Gln	
1853	ĩ				5					10					15		
1854																	
1855	Leu	Thr	Thr	Glu	Thr	Val	Thr	Ile	Va1	Сув	Va1	Ala	Asn	Lys	Phe	Arg	
1856				20					25	_				30		_	
1857																	
1858	Pro	Asn	Asp	Ile	Thr	Val	Thr	Trp	Lys	Val	Asp	Asp	Glu	Ile	Gln	Gln	
1859			35					40					45				
1860																	
1861	Ser	Gly	Phe	Glu	Asn	Ser	Thr	Thr	Pro	Gln	Ser	Pro	G1u	Asp	Cys	Thr	
1862		50					55					60					
1863																	
1864	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Ser	Leu	Thr	Lys	Ala	Gln	Tyr	Asn	Ser	
1865	65					70					75					80	
1866																	
1867	His	Ser	Va1	Tyr	Thr	Сув	Glu	Va1	Val	Hìs	His	Asn	Ser	Gly	Ser	Ala	
1868				-	85	_				90				_	95		
1869																	
1870	Ile	Va1	G1n	Ser	Phe	Asn	Arg	G1y	Asp	Сув							
1871				100					105								
1872																	



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1873																	
1874	(0)																
1875	(2)	) IN	FORM	ATIO	N FO	R SE	2 ID	NO:	45:								
1876		,,		^	<b>~</b> ~ ~			- a m -	<b>aa</b> .			_					
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1878									pair	<u> </u>		$\overline{}$			7	( )	me
1879						nuc							_			_	
1880				-		DEDN:			n								
1881			(1	J) T	OPOL	OGY:	line	ear									
1882		1223					- 537										
1883 1884	(ii) MOLECULE TYPE: cDNA																
1885		(111)	יטיני ו	DOME:	om t A	AT . 1	10										
1886		<b>\</b>	, ai	POIN	51 T C	HT: 1	NO										
1887		/4	AN'	PT _ C 1	DNC 19	. NO											
1888		(10	, AII	11-9	dens	. NO											
1889																	
1890		14	) FE	וסוזייא													
1891		112				KEY:	CDG										
1892						ION:		221									
1893			١.	J, 11	JURI.	2011.		<i>32</i> 1									
1894																	
1895		/v1	SEC	אמדור	ים אי	EGCD.	TDTT!	าพ -	SEQ :	או מד	n.45						
1896		(22.2)		2021				J_11. (	, gur			•					
1897	GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC	ттС	CCA	CCA	TCC	AGT	GAG	CAG	48
1898		Asp															20
1899	1	_			5					10					15	<b></b>	
1900	_				_												
1901	TTA	ACA	TCT	GGA	GGT	GCC	TCA	GTC	GTG	TGC	TTC	TTG	AAC	AAC	TTC	TAC	96
1902		Thr															
1903				20	4				25	-4-				30		-4-	
1904																	
1905	CCC	AAA	GAC	ATC	AAT	GTC	AAG	TGG	AAG	ATT	GAT	GGC	AGT	GAA	CGA	CAA	144
1906		Lys															
1907		•	35				•	40	•		-	•	45		_		
1908																	
1909	AAT	GGC	GTC	CTG	AAC	AGT	TGG	ACT	GAT	CAG	GAC	AGC	AAA	GAC	AGC	ACC	192
1910	Asn	G1y	Va1	Leu	Asn	Ser	Trp	Thr	Asp	G1n	Asp	Ser	Lys	Asp	Ser	Thr	
1911		50					55		_		_	60					
1912																	
1913	TAC	AGC	ATG	AGC	AGC	ACC	CTC	ACG	TTG	ACC	AAG	GAC	GAG	TAT	GAA	CGA	240
1914	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	G1u	Tyr	G1u	Arg	
1915	65					70					75					80	
1916																	
1917	CAT	AAC	AGC	TAT	ACC	TGT	GAG	GCC	ACT	CAC	AAG	ACA	TCA	ACT	TCA	CCC	288
1918		Asn															
1919				-	85					90	-				95		
1920																	
1921	ATT	GTC	AAG	AGC	TTC	AAC	AGG	AAT	GAG	TGT	TA						321
1922	I1e	Va1	Lys	Ser	Phe	Asn	Arg	Asn	G1u	Cys							
1923				100					105								
1924																	

#### Raw Sequence Listing

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1925																
1926	(2)	IN:	FORM	ATIO	N FO	R SE	Q ID	NO:	46:							
1927																
1928			(i):	SEQU	ENCE	CHAI	RACT	ERIS'	rics	:						
1929				(A)	LEI	NGTH	: 10	6 am	ino a	acida	3					
1930				(B)	TY:	PE: a	amino	o ac	id							
1931				(D)	TO:	POLO	GY:	line	ar							
1932																
1933		(:	ii) 1	MOLE	CULE	TYP	E: 10:	rote:	in							
1934		•	·													
1935		(:	xi) :	SEOUI	ENCE	DES	CRIP'	TION	: SEC	מו	NO:	46:				
1936									,	•	_,,					
1937	Ala	Asp	Ala	Ala	Pro	Thr	Va1	Ser	Ile	Phe	Pro	Pro	Ser	Ser	G1u	Gln
1938	1				5					10					15	
1939	_				•											
1940	Leu	Thr	Ser	Glv	Glv	Ala	Ser	Val	Val	Cvs	Phe	T.e.u	Agn	Asn	Phe	Tur
1941				20	<b>-</b> -3				25	O, D				30		-1-
1942				20					25					-		
1943	Pro	T.ve	Asp	T1e	Zen	1/a1	Taye	Tro	Lve	Tla	Agn	@1v	Ser	<b>@1</b> 11	Ara	Gln.
1944		LJ 5	35	110	no	vul	LJ 5	40	<b>п</b> у 5	110	ABP	GLJ	45	914	AL 9	GIII
1945			,,,					10					13			
1946	Agn	Clv	Va1	T.011	Aan	Car	Trn	Thr	Aan	Cl n	a an	Go-	Tara	a an	Car	Thr
1947	ADII	50	741	nea	Apii	Der	55	4111	Abb	G111	ASP	60	пур	App	261	
1948		50										00				
1949	Тъгъ	Sar	Met	Ser	Ser	Thr	T.011	Thr	T.011	Thr	Tare	Aen	Glu	Tur	Gl u	Ara
1950	65	Der	Mec	Der	Der	70	Dea	****	nea	- 111	75	vob	GIG	-7-	GIG	80
1951	03					, 0					73					00
1952	w	*	Ser	П	mb	C	<b>~1</b>	×1 ~	mh	w	T	mh	C 0 = 0	mbs	C 0	D===
1953	UIR	ABII	Ser	ığı	85	CAR	GIU	ATa	Inr	90	пая	TIII	per	TIII	95	PIO
					00					90					93	
1954					-1 -	•			<b>~</b> 3	<b>a</b>						
1955	тте	val	Lys		Phe	Asn	Arg	Asn		cys						
1956				100					105							
1957																

PAGE: 1 SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/952,640 DATE: 06/27/93 TIME: 13:10:31 S5963

LINE ERROR ORIGINAL TEXT

		$\mathcal{Q}$ )
28	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/952640
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
572	Wrong Amino Acid Designator	210 215 (2) INFORMA
592	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
623		Sequence 13 missing
1642	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1726	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
1810	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
1895	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
11	Number of Sequences Doesn't Equal Actual	(iii) NUMBER OF SEQUENCES: 46

PAGE: 1

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/07/952,640

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MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA APPLICATION NUMBER FILING DATE

PAGE:

1

# SEQUENCE CORRECTION REPORT PATENT APPLICATION US/07/952,640

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#### LINE ORIGINAL TEXT

#### 1287 (2) INFORMATION FOR SEQ ID NO:31

1307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

1338 (2) INFORMATION FOR SEQ ID NO:32

1347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

1370 (2) INFORMATION FOR SEQ ID NO:33

1390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

1421 (2) INFORMATION FOR SEQ ID NO:34

1430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

1559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

#### CORRECTED TEXT

(2) INFORMATION FOR SEQ ID NO:31:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

(2) INFORMATION FOR SEQ ID NO:32:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

(2) INFORMATION FOR SEQ ID NO:33:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:33:

(2) INFORMATION FOR SEQ ID NO:34:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37: